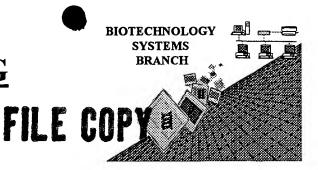
Hill

RAW SEQUENCE LISTING ERROR REPORT



#12

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

1/ // C

Art Unit / Team No.:

3/29/99

Date Processed by STIC:

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

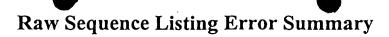
PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212



ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 0.8/

ATTN:	NEW RULES CASES: P	LEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
1	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
2	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
3_/	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces. All text must be visible on page.
4	Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.
5 <u>U</u>	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6	Variable Length	Sequence(s) contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) features section that some may be missing.
7	Wrong Designation	Sequence(s) contain amino acid or nucleic acid designators which are not standard representations as per the Sequence Rules (Please refer to paragraph 1.822)
8	Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped
		Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
9	Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000
	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
	Use of <213>Organism (NEW RULES)	Sequence(s) are missing this mandatory field or its response.
12	Use of <220>Feature (NEW RULES)	Sequence(s) are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Sequence Rules)
13	Patentin ver. 2.0 "bug"	Please do not use "Copy to Disk" function of Patentin version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

, 5, HU++

PAGE: 1

RAW SEQUENCE LISTING PATENT APPLICATION US/08/833,506A

DATE: 03/29/1999 TIME: 08:48:08

INPUT SET: S31225.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Important: Je iten 5 on Euro Summary Sheet SEQUENCE LISTING 1 3 (1) General Information: APPLICANT: ROBERT WEBBER (i) ANTIBODY REACT (ii) TITLE OF INVENTION: IMMUNOASSAY METHOD EMPLOYING MONOCLONAL sel Dan 3 on Erron Summany Held (iii) NUMBER OF SEQUENCES: 126 7 CORRESPONDENCE ADDRESS: (iv) 8 (A) ADDRESSEE: BIELEN, PETERSON & LAMPE 9 (B) STREET: 1990 N. CALIFORNIA BOULEVARD, SUITE 720 10 (C) CITY: WALNUT CREEK Does Not Comply 11 (D) STATE: CALIFORNIA Corrected Diskette Needed (E) COUNTRY: UNITED STATES OF AMERICA 12 13 (F) ZIP: 94596 COMPUTER READABLE FORM: (A) MEDIUM TYPE: DISKETTE 3.5 INCH, 1.44 MB FOR FORMATTED 15 (B) COMPUTER: IBM PC COMPATIBLE 17 (C) OPERATING SYSTEM: DOS (D) SOFTWARE: WORDPERFECT 5.1 18 19 (vi) CURRENT APPLICATION DATA: 20 (A) APPLICATION NUMBER: NONE 21 (B) FILING DATE: NONE 22 (C) CLASSIFICATION: 23 (vii) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: 08/634,332 24 25 (B) FILING DATE: 12 APRIL 1996 (viii) ATTORNEY/AGENT INFORMATION: 26 (A) NAME: THEODORE J. BIELEN, JR. 27 28 (B) REGISTRATION NUMBER: 27,420 29 (C) REFERENCE/DOCKET NUMBER: 12280 30 TELECOMMUNICATION INFORMATION: (ix) TELEPHONE: (925) 937-1515 31 (A) 32 (B) TELEFAX: (925) 937-1529 33 34

ERRORED SEQUENCES FOLLOW:

```
(2) INFORMATION FOR SEQ ID NO: 1:
    (i) SEQUENCE CHARACTERISTICS:
37
     (A) LENGTH: 18
38
     (B) TYPE: AMINO ACID
     (D) TOPOLOGY: LINEAR
```

RAW SEQUENCE LISTING PATENT APPLICATION US/08/833,506A

DATE: 03/29/1999 TIME: 08:48:09

```
40
            (ii) MOLECULE TYPE: PEPTIDE
       41
            (ix) FEATURE:
       42
             (A) NAME/KEY: HUMAN INOS (25-42)
       43
             (B) LOCATION:
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
       44
       45
             (D) OTHER INFORMATION:
       46
                                                               This is due To the use of
This codes between amino
and rumber. Use space.
Caroten, instead.
       47
       48
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
       49
-->
       5.0
            AsnAsnAsnValGluLysAlaProCysAlaThrSerSer
       ⁄51
            510
            ProValThrGlnAsp
       52
       53
            15
       54
       55
       56
                 (2) INFORMATION FOR SEQ ID NO: 2:
       57
            (i) SEQUENCE CHARACTERISTICS:
       58
             (A) LENGTH: 18
       59
             (B) TYPE: AMINO ACID
       60
             (D) TOPOLOGY: LINEAR
            (ii) MOLECULE TYPE: PEPTIDE
       61
       62
            (ix) FEATURE:
       63
                   (A) NAME/KEY: MOUSE iNOS (25-42)
       64
                   (B) LOCATION:
                                                               same end
       65
                   (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
                   (D) OTHER INFORMATION:
       66
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
       67
       68
            AsnAsnAsnValLysLysThrProCysAlaValLeuSer
       69
       70
            ProThrIleGlnAsp
       71
       72
            15
       73
       74
       75
                 (2) INFORMATION FOR SEQ ID NO: 3:
       76
            (i) SEQUENCE CHARACTERISTICS:
       77
             (A) LENGTH: 18
             (B) TYPE: AMINO ACID
       78
       79
             (D) TOPOLOGY: LINEAR
       80
            (ii) MOLECULE TYPE: PEPTIDE
       81
            (ix) FEATURE:
       82
             (A) NAME/KEY: RAT iNOS (25-42)
       83
             (B) LOCATION:
                                                              same
       84
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
       85
             (D) OTHER INFORMATION:
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
       87
            AsnAsnAsnValGluLysThrProGlyAlaIleProSer
       88
       89
            510
            ProThrThrGlnAsp
       90
```

RAW SEQUENCE LISTING PATENT APPLICATION US/08/833,506A

DATE: 03/29/1999 TIME: 08:48:09

```
91
            15
       92
       93
       94
                 (2) INFORMATION FOR SEQ ID NO: 4:
       95
            (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 18
       96
             (B) TYPE: AMINO ACID
       97
       98
             (D) TOPOLOGY: LINEAR
       99
            (ii) MOLECULE TYPE: PEPTIDE
      100
            (ix) FEATURE:
             (A) NAME/KEY: HUMAN INOS (37-54)
      101
      102
             (B) LOCATION:
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      103
             (D) OTHER INFORMATION:
      104
      105
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
      106
      107
            SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
      108
            510
      109
            SerLysGlnGlnAsn
      110
            15
      111
      112
      113
                 (2) INFORMATION FOR SEQ ID NO: 5:
      114
            (i) SEQUENCE CHARACTERISTICS:
      115
             (A) LENGTH: 18
      116
             (B) TYPE: AMINO ACID
      117
             (D) TOPOLOGY: LINEAR
      118
            (ii) MOLECULE TYPE: PEPTIDE
      119
            (ix) FEATURE:
      120
             (A) NAME/KEY: HUMAN iNOS (781-798)
      121
             (B) LOCATION:
      122
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      123
             (D) OTHER INFORMATION:
      124
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
      125
      126
            ProAlaLeuValGlnGlyIleLeuGluArgValValAsp
      127
            510
      128
            GlyProThrProHis
      129
      130
      131
      132
                 (2) INFORMATION FOR SEQ ID NO: 6:
      133
            (i) SEQUENCE CHARACTERISTICS:
      134
             (A) LENGTH: 17
-->
      135
             (B) TYPE: AMINO ACID
      136
             (D) TOPOLOGY: LINEAR
      137
            (ii) MOLECULE TYPE: PEPTIDE
      138
            (ix) FEATURE:
             (A) NAME/KEY: MOUSE INOS (776-792)
      139
      140
             (B) LOCATION:
```

RAW SEQUENCE LISTING PATENT APPLICATION US/08/833,506A

DATE: 03/29/1999 TIME: 08:48:09

```
141
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      142
             (D) OTHER INFORMATION:
      143
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                      Same
      144
      145
            XaaAlaLeuValGlnGlyIleLeuGluArgValValAsp
      146
            510
      147
            CysProThrProHis
      148
            15
      149
      150
      151
      152
                 (2) INFORMATION FOR SEQ ID NO: 7:
      153
            (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 15
      154
-->
      155
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR
      156
            (ii) MOLECULE TYPE: PEPTIDE
      157
      158
            (ix) FEATURE:
      159
             (A) NAME/KEY: RAT iNOS (780-794)
             (B) LOCATION:
      160
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      161
      162
             (D) OTHER INFORMATION:
      163
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
      164
      165
            XaaXaaLeuValGlnGlyIleLeuGluArgValValAsp
      166
            510
      167
            CysSerSerProXaa
      168
            15
      169
      170
      171
                 (2) INFORMATION FOR SEQ ID NO: 8:
      172
            (i) SEQUENCE CHARACTERISTICS:
      173
             (A) LENGTH: 18
      174
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR
      175
      176
            (ii) MOLECULE TYPE: PEPTIDE
            (ix) FEATURE:
      177
      178
             (A) NAME/KEY: HUMAN iNOS (985-1002)
      179
             (B) LOCATION:
      180
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      181
             (D) OTHER INFORMATION:
      182
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
      183
      184
            GlyIleValProPheArgSerPheTrpGlnGlnArgLeu
      185
      186
            HisAspSerGlnHis
      187
      188
      189
```

RAW SEQUENCE LISTING PATENT APPLICATION US/08/833,506A

DATE: 03/29/1999 TIME: 08:48:10

```
191
            (i) SEQUENCE CHARACTERISTICS:
      192
             (A) LENGTH: 18
      193
             (B) TYPE: AMINO ACID
      194
             (D) TOPOLOGY: LINEAR
      195
            (ii) MOLECULE TYPE: PEPTIDE
                                                                   Same
            (ix) FEATURE:
      196
      197
             (A) NAME/KEY: MOUSE INOS (978-995)
      198
             (B) LOCATION:
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      199
      200
             (D) OTHER INFORMATION:
      201
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
      202
      203
            GlyIleAlaProPheArgSerPheTrpGlnGlnArgLeu
      204
      205
            510
      206
            HisAspSerGlnHis
      207
            15
      208
      209
      210
                 (2) INFORMATION FOR SEQ ID NO: 10:
      211
            (i) SEQUENCE CHARACTERISTICS:
      212
             (A) LENGTH: 18
             (B) TYPE: AMINO ACID
      213
      214
             (D) TOPOLOGY: LINEAR
      215
            (ii) MOLECULE TYPE: PEPTIDE
      216
            (ix) FEATURE:
             (A) NAME/KEY: RAT INOS (982-998)
      217
             (B) LOCATION:
      218
      219
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      220
             (D) OTHER INFORMATION:
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
      221
      222
      223
            GlyIleAlaProPheArgSerPheTrpGlnGlnArgLeu510
      224
           HisAspSerGlnHis
      225
      226
      227
      228
                 (2) INFORMATION FOR SEQ ID NO: 11:
      229
            (i) SEQUENCE CHARACTERISTICS:
      230
             (A) LENGTH: 18
-->
      231
             (B) TYPE: AMINO ACID
      232
             (D) TOPOLOGY: LINEAR
            (ii) MOLECULE TYPE: PEPTIDE
      233
      234
            (ix) FEATURE:
      235
             (A) NAME/KEY: HUMAN nNOS (1256-1273)
      236
             (B) LOCATION:
      237
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      238
             (D) OTHER INFORMATION:
      239
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
      240
      241
           GlyIleAlaProPheArgSerPheTrpGlnGlnArgGln
```

RAW SEQUENCE LISTING PATENT APPLICATION US/08/833,506A

DATE: 03/29/1999 TIME: 08:48:10

```
242
                                                                           same
      243
            PheAspIleGlnHis
      244
      245
      246
      247
                 (2) INFORMATION FOR SEQ ID NO: 12:
      248
            (i) SEQUENCE CHARACTERISTICS:
      249
             (A) LENGTH: 15
      250
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR
      251
            (ii) MOLECULE TYPE: PEPTIDE
      252
            (ix) FEATURE:
      253
                  (A) NAME/KEY: HUMAN eNOS (1017-1031)
      254
      255
                  (B) LOCATION:
                  (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      256
      257
                  (D) OTHER INFORMATION:
      258
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
      259
            GlyIleAlaProPheArgGlyPheTrpGlnGluArgLeu
      260
      261
            510
      262
            HisAspXaaXaaXaa
      263
      264
      265
      266
                 (2) INFORMATION FOR SEQ ID NO: 13:
            (i) SEQUENCE CHARACTERISTICS:
      267
             (A) LENGTH: 15
      268
-->
             (B) TYPE: AMINO ACID
      269
             (D) TOPOLOGY: LINEAR
      270
            (ii) MOLECULE TYPE: PEPTIDE
      271
      272
            (ix) FEATURE:
      273
             (A) NAME/KEY: BOVINE eNOS (1019-1033)
      274
             (B) LOCATION:
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      275
             (D) OTHER INFORMATION:
      276
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
      277
      278
      279
            GlyIleAlaProPheArgGlyPheTrpGlnGluArgLeu
      280
            510
      281
            HisAspXaaXaaXaa
-->
      282
            15
      283
      284
      285
                 (2) INFORMATION FOR SEQ ID NO: 14:
      286
            (i) SEQUENCE CHARACTERISTICS:
      287
             (A) LENGTH: 18
      288
             (B) TYPE: AMINO ACID
      289
             (D) TOPOLOGY: LINEAR
            (ii) MOLECULE TYPE: PEPTIDE
      290
            (ix) FEATURE:
      291
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/833,506A

DATE: 03/29/1999 TIME: 08:48:10

```
292
             (A) NAME/KEY: HUMAN iNOS (1009-1026)
      293
             (B) LOCATION:
      294
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
                                                                        /same
      295
             (D) OTHER INFORMATION:
      296
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
      297
      298
            ArgMetThrLeuValPheGlyCysArgArgProAspGlu
      299
            510
            AspHisIleTyrGln
      300
      301
      302
      303
      304
                 (2) INFORMATION FOR SEQ ID NO: 15:
      305
            (i) SEQUENCE CHARACTERISTICS:
      306
             (A) LENGTH: 18
      307
             (B) TYPE: AMINO ACID
      308
             (D) TOPOLOGY: LINEAR
      309
            (ii) MOLECULE TYPE: PEPTIDE
      310
            (ix) FEATURE:
             (A) NAME/KEY: RAT INOS (1006-1023)
      311
      312
             (B) LOCATION:
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      313
      314
             (D) OTHER INFORMATION:
      315
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
      316
            ArgMetThrLeuValPheGlyCysArgHisProGluGlu
      317
      318
      319
            AspHisLeuTyrGln
      320
            15
      321
      322
      323
                 (2) INFORMATION FOR SEQ ID NO: 16:
      324
            (i) SEQUENCE CHARACTERISTICS:
      325
             (A) LENGTH: 18
      326
             (B) TYPE: AMINO ACID
      327
             (D) TOPOLOGY: LINEAR
      328
            (ii) MOLECULE TYPE: PEPTIDE
      329
            (ix) FEATURE:
             (A) NAME/KEY: MOUSE iNOS (1002-1019)
      .330
      331
             (B) LOCATION:
      332
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      333
             (D) OTHER INFORMATION:
      334
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
      335
      336
            ArgMetSerLeuValPheGlyCysArgHisProGluGlu
-->
      337
            510
-->
      338
            AspHisLeuTyrGln
      339
      340
      341
```

RAW SEQUENCE LISTING PATENT APPLICATION US/08/833,506A

DATE: 03/29/1999 TIME: 08:48:11

```
343
            (i) SEQUENCE CHARACTERISTICS:
-->
      344
             (A) LENGTH: 16
      345
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR
      346
      347
            (ii) MOLECULE TYPE: PEPTIDE
      348
            (ix) FEATURE:
             (A) NAME/KEY: hnNOS [2-16, Cys17]
      349
      350
             (B) LOCATION: HUMAN NNOS: AMINO TERMINAL
      351
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      352
             (D) OTHER INFORMATION:
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
      353
      354
      355
            GluAspHisMetPheGlyValGlnGlnIleGlnProAsn
      356
            510
      357
            VallleCys
      358
            15
      359
      360
                 (2) INFORMATION FOR SEQ ID NO: 18:
      361
            (i) SEQUENCE CHARACTERISTICS:
      362
             (A) LENGTH: 24
-->
             (B) TYPE: AMINO ACID
      363
      364
             (D) TOPOLOGY: LINEAR
      365
            (ii) MOLECULE TYPE: PEPTIDE
      366
            (ix) FEATURE:
             (A) NAME/KEY: hnNOS [Cys1410-1411-1433]
             (B) LOCATION: HUMAN NNOS: CARBOXYL TERMINAL
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      369
      370
             (D) OTHER INFORMATION:
      371
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
      372
      373
            CysArgLeuArgSerGluSerIleAlaPheIleGluGlu
      374
            SerLysLysAspThrAspGluValPheSerSer
      375
      376
            1520
      377
      378
      379
                 (2) INFORMATION FOR SEQ ID NO: 19:
      380
            (i) SEQUENCE CHARACTERISTICS:
      381
             (A) LENGTH: 20
      382
             (B) TYPE: AMINO ACID
      383
             (D) TOPOLOGY: LINEAR
      384
            (ii) MOLECULE TYPE: PEPTIDE
      385
            (ix) FEATURE:
      386
             (A) NAME/KEY: hinos [2-21, Ser2]
      387
             (B) LOCATION: HUMAN INOS: AMINO TERMINAL
      388
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      389
             (D) OTHER INFORMATION:
      390
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
      391
      392
            AlaSerProTrpLysPheLeuPheLysThrLysPheHis
      393
            510
```

RAW SEQUENCE LISTING PATENT APPLICATION US/08/833,506A

DATE: 03/29/1999 TIME: 08:48:11

```
394
            GlnTyrAlaMetAsnGlyGlu
                                                                           sane
      395
            1520
      396
      397
      398
                 (2) INFORMATION FOR SEQ ID NO: 20:
      399
            (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 18
      400
             (B) TYPE: AMINO ACID
      401
             (D) TOPOLOGY: LINEAR
      402
      403
            (ii) MOLECULE TYPE: PEPTIDE
            (ix) FEATURE:
      404
             (A) NAME/KEY: hiNOS [Cysl136-1137-1153]
      405
             (B) LOCATION: HUMAN INOS: CARBOXYL TERMINAL
      406
      407
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      408
             (D) OTHER INFORMATION:
      409
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
      410
      411
            CysLysLysAspArgValAlaValGlnProSerSerLeu
      412
      413
            510
            GluMetSerAlaLeu
      414
      415
            15
      416
      417
      418
                 (2) INFORMATION FOR SEQ ID NO: 21:
      419
            (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 12
      420
             (B) TYPE: AMINO ACID
      421
             (D) TOPOLOGY: LINEAR
      422
            (ii) MOLECULE TYPE: PEPTIDE
      423
            (ix) FEATURE:
      424
      425
             (A) NAME/KEY: heNOS [Cap-2-12, Cys13]
             (B) LOCATION: HUMAN eNOS: AMINO TERMINAL WITH CAPROIC ACID ATTACHED
      426
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      427
      428
             (D) OTHER INFORMATION:
      429
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:
      430
      431
            GlyAsnLeuLysSerValAlaGlnGluProGlyCys
      432
      433
      434
      435
                 (2) INFORMATION FOR SEQ ID NO: 22:
            (i) SEQUENCE CHARACTERISTICS:
      436
      437
-->
             (A) LENGTH: 12
      438
             (B) TYPE: AMINO ACID
      439
             (D) TOPOLOGY: LINEAR
      440
            (ii) MOLECULE TYPE: PEPTIDE
      441
            (ix) FEATURE:
      442
             (A) NAME/KEY: heNOS [2-12, Cys13]
             (B) LOCATION: HUMAN eNOS: AMINO TERMINAL WITHOUT CAPROIC ACID ATTACHED
      443
```

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```
444
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      445
             (D) OTHER INFORMATION:
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
      446
                                                                     same
      447
      448
           GlyAsnLeuLysSerValAlaGlnGluProGlyCys
      449
           510
      450
      451
      452
                 (2) INFORMATION FOR SEQ ID NO: 23:
      453
            (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 23
      454
      455
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR
      456
      457
            (ii) MOLECULE TYPE: PEPTIDE
      458
            (ix) FEATURE:
      459
             (A) NAME/KEY: heNOS [Cys1181-1182-1203]
             (B) LOCATION: HUMAN eNOS: CARBOXYL TERMINAL
      460
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      461
      462
             (D) OTHER INFORMATION:
      463
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:
      464
      465
           CysGluArgGlnLeuArgGluAlaValProTrpAlaPhe
      466
      467
           AspProProGlySerAspThrAsnSerPro
      468
           1520
      469
      470
                 (2) INFORMATION FOR SEQ ID NO: 24:
      471
            (i) SEQUENCE CHARACTERISTICS:
      472
      473
             (A) LENGTH: 18
-->
             (B) TYPE: AMINO ACID
      474
      475
             (D) TOPOLOGY: LINEAR
            (ii) MOLECULE TYPE: PEPTIDE
      476
      477
            (ix) FEATURE:
      478
             (A) NAME/KEY: hinos [985-1002]
      479
             (B) LOCATION:
      480
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      481
             (D) OTHER INFORMATION:
      482
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:
      483
      484
           GlyIleValProPheArgSerPheTrpGlnGlnArgLeu
      485
           510
      486
           HisAspSerGlnHis
      487
           15
      488
      489
      490
                 (2) INFORMATION FOR SEQ ID NO: 25:
      491
            (i) SEQUENCE CHARACTERISTICS:
      492
             (A) LENGTH: 18
      493
             (B) TYPE: AMINO ACID
```

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```
494
             (D) TOPOLOGY: LINEAR
      495
            (ii) MOLECULE TYPE: PEPTIDE
                                                                       same
            (ix) FEATURE:
      496
             (A) NAME/KEY: hiNOS [985-1002]
      497
      498
             (B) LOCATION:
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      499
      500
             (D) OTHER INFORMATION:
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:
      501
      502
      503
            GlyIleValProPheArgSerPheTrpGlnGlnArgLeu
      504
            510
      505
            His AspSerGlnHis
      506
      507
      508
      509
                 (2) INFORMATION FOR SEQ ID NO: 26:
      510
            (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 18
-->
      511
      512
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR
      513
            (ii) MOLECULE TYPE: PEPTIDE
      514
      515
            (ix) FEATURE:
      516
             (A) NAME/KEY: hiNOS [37-54]
      517
             (B) LOCATION:
      518
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      519
             (D) OTHER INFORMATION:
      520
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:
      521
            SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
      522
      523
            510
            SerLysGlnGlnAsn
      524
      525
            15
      526
      527
                 (2) INFORMATION FOR SEQ ID NO: 27:
      528
      529
            (i) SEQUENCE CHARACTERISTICS:
      530
             (A) LENGTH: 18
      531
             (B) TYPE: AMINO ACID
      532
             (D) TOPOLOGY: LINEAR
      533
            (ii) MOLECULE TYPE: PEPTIDE
            (ix) FEATURE:
      534
      535
             (A) NAME/KEY: hiNOS [781-798]
      536
             (B) LOCATION:
      537
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      538
             (D) OTHER INFORMATION:
      539
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:
      540
      541
            ProAlaLeuValGlnGlyIleLeuGluArgValValAsp
      542
            510
      543
            GlyProThrProHis
      544
```

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```
545
            15
      546
      547
                 (2) INFORMATION FOR SEQ ID NO: 28:
      548
      549
            (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 18
      550
             (B) TYPE: AMINO ACID
      551
             (D) TOPOLOGY: LINEAR
      552
      553
            (ii) MOLECULE TYPE: PEPTIDE
            (ix) FEATURE:
      554
             (A) NAME/KEY: hiNOS [25-42]
      555
      556
             (B) LOCATION:
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      557
             (D) OTHER INFORMATION:
      558
      559
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:
      560
      561
            AsnAsnAsnValGluLysAlaProSerAlaThrSerSer
      562
            510
            ProValThrGlnAsp
      563
      564
            15
      565
      566
      567
                 (2) INFORMATION FOR SEQ ID NO: 29:
            (i) SEQUENCE CHARACTERISTICS:
      568
             (A) LENGTH: 18
      569
             (B) TYPE: AMINO ACID
      570
             (D) TOPOLOGY: LINEAR
      571
            (ii) MOLECULE TYPE: PEPTIDE
      572
            (ix) FEATURE:
      573
             (A) NAME/KEY: hinos [37-54]
      574
      575
             (B) LOCATION:
      576
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      577
             (D) OTHER INFORMATION:
      578
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:
      579
            SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
      580
      581
            510
      582
            SerLysGlnGlnAsn
      583
      584
      585
      586
                 (2) INFORMATION FOR SEQ ID NO: 30:
            (i) SEQUENCE CHARACTERISTICS:
      587
-->
      588
             (A) LENGTH: 18
      589
             (B) TYPE: AMINO ACID
      590
             (D) TOPOLOGY: LINEAR
      591
            (ii) MOLECULE TYPE: PEPTIDE
            (ix) FEATURE:
      592
             (A) NAME/KEY: hiNOS [781-798]
      593
      594
             (B) LOCATION:
```

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```
595
       (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
596
       (D) OTHER INFORMATION:
597
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:
598
                                                                   same
599
     ProAlaLeuValGlnGlyIleLeuGluArgValValAsp
600
     510
601
     GlyProThrProHis
602
     15
603
604
605
           (2) INFORMATION FOR SEQ ID NO: 31:
     (i) SEQUENCE CHARACTERISTICS:
606
607
       (A) LENGTH: 18
608
       (B) TYPE: AMINO ACID
609
       (D) TOPOLOGY: LINEAR
     (ii) MOLECULE TYPE: PEPTIDE
610
611
     (ix) FEATURE:
612
       (A) NAME/KEY: hiNOS [1009-1026]
613
       (B) LOCATION:
       (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
614
615
       (D) OTHER INFORMATION:
616
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:
617
618
619
     ArgMetThrLeuValPheGlySerArgArgProAspGlu
620
     510
621
     AspHisIleTyrGln
622
     15
623
624
           (2) INFORMATION FOR SEQ ID NO: 32:
625
626
     (i) SEQUENCE CHARACTERISTICS:
627
       (A) LENGTH: 18
628
       (B) TYPE: AMINO ACID
629
       (D) TOPOLOGY: LINEAR
     (ii) MOLECULE TYPE: PEPTIDE
630
631
     (ix) FEATURE:
632
            (A) NAME/KEY: (A3) LOCUS HUMAN iNOS (25-42)
633
            (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
634
            (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
635
            (D) OTHER INFORMATION:
636
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:
637
638
     AsnAsnAsnValGluLysAlaProSerAlaThrSerSer
639
640
     ProValThrGlnAsp
641
642
643
```

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```
645
            (i) SEQUENCE CHARACTERISTICS:
-->
      646
             (A) LENGTH: 18
      647
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR
      648
                                                                          sane
            (ii) MOLECULE TYPE: PEPTIDE
      649
      650
            (ix) FEATURE:
             (A) NAME/KEY: MOUSE INOS (25-42)
      651
      652
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      653
      654
             (D) OTHER INFORMATION:
      655
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:
      656
      657
            AsnAsnAsnValLysLysThrProSerAlaValLeuSer
      658
            510
      659
            ProThrIleGlnAsp
      660
            15
      661
      662
      663
                 (2) INFORMATION FOR SEQ ID NO: 34:
            (i) SEQUENCE CHARACTERISTICS:
      664
             (A) LENGTH: 18
      665
             (B) TYPE: AMINO ACID
      666
             (D) TOPOLOGY: LINEAR
      667
      668
            (ii) MOLECULE TYPE: PEPTIDE
      669
            (ix) FEATURE:
      670
             (A) NAME/KEY: RAT INOS (25-42)
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
      671
      672
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      673
             (D) OTHER INFORMATION:
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
      674
      675
      676
            AsnAsnAsnValGluLysThrProGlyAlaIleProSer
      677
      678
            ProThrThrGlnAsp
      679
      680
      681
      682
                 (2) INFORMATION FOR SEQ ID NO: 35:
      683
            (i) SEQUENCE CHARACTERISTICS:
      684
             (A) LENGTH: 15
-->
      685
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR
      686
            (ii) MOLECULE TYPE: PEPTIDE
      687
      688
            (ix) FEATURE:
      689
             (A) NAME/KEY: HUMAN iNOS (28-42)
      690
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
      691
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      692
            (D) OTHER INFORMATION:
      693
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:
      694
      695
            ValGluLysAlaProSerAlaThrSerSerProValThr
```

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```
696
            510
      697
            GlnAsp
                                                                       same
      698
            15
      699
      700
      701
                 (2) INFORMATION FOR SEQ ID NO: 36:
      702
            (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 12
      703
      704
             (B) TYPE: AMINO ACID
                                                                            Sane
             (D) TOPOLOGY: LINEAR
      705
      706
            (ii) MOLECULE TYPE: PEPTIDE
      707
            (ix) FEATURE:
      708
             (A) NAME/KEY: HUMAN iNOS (31-42)
      709
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      710
      711
             (D) OTHER INFORMATION:
      712
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:
      713
            AlaProSerAlaThrSerSerProValThrGlnAsp
-->
      714
      715
            510
      716
      717
      718
                 (2) INFORMATION FOR SEQ ID NO: 37:
            (i) SEQUENCE CHARACTERISTICS:
      719
-->
      720
             (A) LENGTH: 9
             (B) TYPE: AMINO ACID
      721
      722
             (D) TOPOLOGY: LINEAR
            (ii) MOLECULE TYPE: PEPTIDE
      723
            (ix) FEATURE:
      724
      725
             (A) NAME/KEY: HUMAN iNOS (34-42)
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
      726
      727
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      728
             (D) OTHER INFORMATION:
      729
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:
      730
           AlaThrSerSerProValThrGlnAsp
      731
-->
      732
      733
      734
      735
                 (2) INFORMATION FOR SEQ ID NO: 38:
            (i) SEQUENCE CHARACTERISTICS:
      736
      737
             (A) LENGTH: 6
-->
      738
             (B) TYPE: AMINO ACID
      739
             (D) TOPOLOGY: LINEAR
      740
            (ii) MOLECULE TYPE: PEPTIDE
      741
            (ix) FEATURE:
      742
             (A) NAME/KEY: HUMAN iNOS (37-42)
      743
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
      744
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      745
             (D) OTHER INFORMATION:
```

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```
746
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:
747
748
     SerProValThrGlnAsp
                                                                 some
749
750
751
752
           (2) INFORMATION FOR SEQ ID NO: 39:
753
      (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 15
754
755
       (B) TYPE: AMINO ACID
756
       (D) TOPOLOGY: LINEAR
757
      (ii) MOLECULE TYPE: PEPTIDE
758
      (ix) FEATURE:
       (A) NAME/KEY: HUMAN iNOS (25-39)
759
760
       (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
       (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
761
762
       (D) OTHER INFORMATION:
763
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:
764
     AsnAsnAsnValGluLysAlaProSerAlaThrSerSer
765
766
     510
     ProVal
767
768
     15
769
770
           (2) INFORMATION FOR SEQ ID NO: 40:
771
772
      (i) SEQUENCE CHARACTERISTICS:
773
       (A) LENGTH: 12
       (B) TYPE: AMINO ACID
774
       (D) TOPOLOGY: LINEAR
775
776
      (ii) MOLECULE TYPE: PEPTIDE
777
      (ix) FEATURE:
778
       (A) NAME/KEY: HUMAN iNOS (25-36)
779
       (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
780
       (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
       (D) OTHER INFORMATION:
781
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:
782
783
784
     AsnAsnAsnValGluLysAlaProSerAlaThrSer
785
     510
786
787
788
           (2) INFORMATION FOR SEQ ID NO: 41:
789
     (i) SEQUENCE CHARACTERISTICS:
790
       (A) LENGTH: 9
791
      (B) TYPE: AMINO ACID
792
      (D) TOPOLOGY: LINEAR
793
     (ii) MOLECULE TYPE: PEPTIDE
794
     (ix) FEATURE:
795
      (A) NAME/KEY: HUMAN INOS (25-33)
```

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```
(B) LOCATION: CARBOXY TERMINAL WITH AMIDE
      797
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
                                                                         sane
      798
             (D) OTHER INFORMATION:
      799
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:
      800
      801
            AsnAsnAsnValGluLysAlaProSer
      802
      803
      804
      805
                 (2) INFORMATION FOR SEQ ID NO: 42:
      806
            (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 6
-->
      807
             (B) TYPE: AMINO ACID
      808
      809
             (D) TOPOLOGY: LINEAR
            (ii) MOLECULE TYPE: PEPTIDE
      810
      811
            (ix) FEATURE:
      812
                  (A) NAME/KEY: HUMAN INOS (25-30)
      813
                  (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
      814
                  (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      815
                  (D) OTHER INFORMATION:
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:
      816
      817
            AsnAsnAsnValGluLys
      818
      819
      820
      821
                 (2) INFORMATION FOR SEQ ID NO: 43:
      822
      823
            (i) SEQUENCE CHARACTERISTICS:
      824
             (A) LENGTH: 18
      825
             (B) TYPE: AMINO ACID
      826
             (D) TOPOLOGY: LINEAR
            (ii) MOLECULE TYPE: PEPTIDE
      827
      828
            (ix) FEATURE:
      829
             (A) NAME/KEY: (A4) LOCUS HUMAN INOS (37-54)
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
      830
      831
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      832
             (D) OTHER INFORMATION:
      833
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:
      834
      835
            SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
      836
      837
            SerLysGlnGlnAsn
      838
      839
      840
      841
                 (2) INFORMATION FOR SEQ ID NO: 44:
      842
            (i) SEQUENCE CHARACTERISTICS:
      843
             (A) LENGTH: 15
             (B) TYPE: AMINO ACID
      844
      845
             (D) TOPOLOGY: LINEAR
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846
     (ii) MOLECULE TYPE: PEPTIDE
847
     (ix) FEATURE:
848
       (A) NAME/KEY: HUMAN INOS (40-54)
       (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
849
       (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
850
851
       (D) OTHER INFORMATION:
                                                               Spri
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:
852
853
854
     ThrGlnAspAspLeuGlnTyrHisAsnLeuSerLysGln
855
     510
856
     GlnAsn
857
     15
858
859
           (2) INFORMATION FOR SEQ ID NO: 45:
860
861
     (i) SEQUENCE CHARACTERISTICS:
862
       (A) LENGTH: 12
863
      (B) TYPE: AMINO ACID
864
      (D) TOPOLOGY: LINEAR
     (ii) MOLECULE TYPE: PEPTIDE
865
866
     (ix) FEATURE:
       (A) NAME/KEY: HUMAN iNOS (43-54)
867
       (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
868
      (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
869
870
      (D) OTHER INFORMATION:
871
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:
872
873
     AspLeuGlnTyrHisAsnLeuSerLysGlnGlnAsn
874
     510
875
876
877
878
           (2) INFORMATION FOR SEQ ID NO: 46:
880
     (i) SEQUENCE CHARACTERISTICS:
881
       (A) LENGTH: 9
882
       (B) TYPE: AMINO ACID
883
      (D) TOPOLOGY: LINEAR
884
     (ii) MOLECULE TYPE: PEPTIDE
885
     (ix) FEATURE:
886
       (A) NAME/KEY: HUMAN iNOS (46-54)
887
       (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
888
      (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
889
      (D) OTHER INFORMATION:
890
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:
891
892
     TyrHisAsnLeuSerLysGlnGlnAsn
893
     5
894
895
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897
            (i) SEQUENCE CHARACTERISTICS:
-->
      898
             (A) LENGTH: 6
      899
             (B) TYPE: AMINO ACID
      900
             (D) TOPOLOGY: LINEAR
      901
            (ii) MOLECULE TYPE: PEPTIDE
      902
            (ix) FEATURE:
      903
             (A) NAME/KEY: HUMAN INOS (49-54)
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
      904
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      905
      906
             (D) OTHER INFORMATION:
      907
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:
      908
      909
            LeuSerLysGlnGlnAsn
-->
      910
      911
      912
      913
                 (2) INFORMATION FOR SEQ ID NO: 48:
            (i) SEQUENCE CHARACTERISTICS:
      914
             (A) LENGTH: 15
      915
             (B) TYPE: AMINO ACID
      916
             (D) TOPOLOGY: LINEAR
      917
      918
            (ii) MOLECULE TYPE: PEPTIDE
            (ix) FEATURE:
      919
      920
             (A) NAME/KEY: HUMAN iNOS (37-51)
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
      921
      922
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      923
             (D) OTHER INFORMATION:
      924
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:
      925
      926
            SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
      927
            510
            SerLys
      928
      929
            15
      930
      931
      932
                 (2) INFORMATION FOR SEQ ID NO: 49:
      933
            (i) SEQUENCE CHARACTERISTICS:
      934
             (A) LENGTH: 12
-->
      935
             (B) TYPE: AMINO ACID
      936
             (D) TOPOLOGY: LINEAR
      937
            (ii) MOLECULE TYPE: PEPTIDE
      938
            (ix) FEATURE:
             (A) NAME/KEY: HUMAN INOS (37-48)
      939
      940
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
      941
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      942
             (D) OTHER INFORMATION:
      943
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:
      944
-->
      945
            SerProValThrGlnAspAspLeuGlnTyrHisAsn
      946
            510
      947
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/833,506A

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948
949
           (2) INFORMATION FOR SEQ ID NO: 50:
950
      (i) SEQUENCE CHARACTERISTICS:
951
       (A) LENGTH: 9
952
       (B) TYPE: AMINO ACID
953
      (D) TOPOLOGY: LINEAR
954
      (ii) MOLECULE TYPE: PEPTIDE
955
      (ix) FEATURE:
956
      (A) NAME/KEY: HUMAN iNOS (37-45)
957
       (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
958
      (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
959
      (D) OTHER INFORMATION:
960
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:
961
     SerProValThrGlnAspAspLeuGln
962
963
964
965
           (2) INFORMATION FOR SEQ ID NO: 51:
966
967
      (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 6
968
      (B) TYPE: AMINO ACID
969
      (D) TOPOLOGY: LINEAR
970
971
      (ii) MOLECULE TYPE: PEPTIDE
972
      (ix) FEATURE:
973
      (A) NAME/KEY: HUMAN iNOS (37-42)
974
      (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
975
      (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
976
      (D) OTHER INFORMATION:
977
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:
978
979
     SerProValThrGlnAsp
980
981
982
983
984
           (2) INFORMATION FOR SEQ ID NO: 52:
985
      (i) SEQUENCE CHARACTERISTICS:
986
      (A) LENGTH: 18
987
      (B) TYPE: AMINO ACID
988
      (D) TOPOLOGY: LINEAR
      (ii) MOLECULE TYPE: PEPTIDE
989
     (ix) FEATURE:
990
      (A) NAME/KEY: (F6) LOCUS HUMAN iNOS (781-798)
991
992
      (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
993
      (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
994
      (D) OTHER INFORMATION:
995
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:
996
997
     ProAlaLeuValGlnGlyIleLeuGluArgValValAsp
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/833,506A

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INPUT SET: S31225.raw 998 sane GlyProThrProHis --> 999 1000 15 1001 1002 (2) INFORMATION FOR SEQ ID NO: 53: 1003 1004 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 1005 (B) TYPE: AMINO ACID 1006 1007 (D) TOPOLOGY: LINEAR 1008 (ii) MOLECULE TYPE: PEPTIDE (ix) FEATURE: 1009 (A) NAME/KEY: HUMAN eNOS (806-824) 1010 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE 1011 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS 1012 (D) OTHER INFORMATION: 1013 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53: 1014 1015 1016 ProGlyLeuValGluAlaLeuLeuSerArgValGluAsp 1017 ProProAlaProThrGlu 1018 1019 1020 1021 1022 (2) INFORMATION FOR SEQ ID NO: 54: 1023 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 1024 1025 (B) TYPE: AMINO ACID (D) TOPOLOGY: LINEAR 1026 1027 (ii) MOLECULE TYPE: PEPTIDE 1028 (ix) FEATURE: 1029 (A) NAME/KEY: HUMAN INOS (784-798) (B) LOCATION: CARBOXY TERMINAL WITH AMIDE 1030 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS 1031 (D) OTHER INFORMATION: 1032 1033 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54: 1034 1035 1036 ValGlnGlyIleLeuGluArgValValAspGlyProThr 1037 510 1038 ProHis 1039 15 1040 1041 1042 (2) INFORMATION FOR SEQ ID NO: 55: 1043 (i) SEQUENCE CHARACTERISTICS:

--> 1044 (A) LENGTH: 12

1045 (B) TYPE: AMINO ACID

1046 (D) TOPOLOGY: LINEAR

1047 (ii) MOLECULE TYPE: PEPTIDE

RAW SEQUENCE LISTING PATENT APPLICATION US/08/833,506A

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(ix) FEATURE:
1048
        (A) NAME/KEY: HUMAN INOS (787-798)
1049
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1050
1051
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
                                                                   Jane
1052
        (D) OTHER INFORMATION:
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:
1053
1054
1055
       IleLeuGluArgValValAspGlyProThrProHis
1056
       510
1057
1058
            (2) INFORMATION FOR SEQ ID NO: 56:
1059
1060
       (i) SEQUENCE CHARACTERISTICS:
1061
        (A) LENGTH: 9
        (B) TYPE: AMINO ACID
1062
        (D) TOPOLOGY: LINEAR
1063
1064
       (ii) MOLECULE TYPE: PEPTIDE
       (ix) FEATURE:
1065
        (A) NAME/KEY: HUMAN iNOS (790-798)
1066
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1067
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1068
1069
        (D) OTHER INFORMATION:
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:
1070
1071
      ArgValValAspGlyProThrProHis
1072
1073
1074
1075
            (2) INFORMATION FOR SEQ ID NO: 57:
1076
1077
       (i) SEQUENCE CHARACTERISTICS:
1078
        (A) LENGTH: 6
1079
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR
1080
1081
       (ii) MOLECULE TYPE: PEPTIDE
1082
       (ix) FEATURE:
1083
        (A) NAME/KEY: HUMAN INOS (793-798)
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1084
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1085
1086
        (D) OTHER INFORMATION:
1087
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:
1088
1089
      AspGlyProThrProHis
1090
1091
1092
1093
            (2) INFORMATION FOR SEQ ID NO: 58:
       (i) SEQUENCE CHARACTERISTICS:
1094
1095
        (A) LENGTH: 14
1096
        (B) TYPE: AMINO ACID
1097
        (D) TOPOLOGY: LINEAR
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1147

(A) LENGTH: 6

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```
1098
            (ii) MOLECULE TYPE: PEPTIDE
     1099
            (ix) FEATURE:
     1100
             (A) NAME/KEY: HUMAN iNOS (781-794)
     1101
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
     1102
     1103
             (D) OTHER INFORMATION:
    1104
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:
     1105
            ProAlaLeuValGlnGlyIleLeuGluArgValValAsp
-->
     1106
     1107
     1108
            Gly
     1109
     1110
     1111
                 (2) INFORMATION FOR SEQ ID NO: 59:
            (i) SEQUENCE CHARACTERISTICS:
     1112
     1113
             (A) LENGTH: 12
     1114
             (B) TYPE: AMINO ACID
     1115
             (D) TOPOLOGY: LINEAR
     1116
            (ii) MOLECULE TYPE: PEPTIDE
     1117
            (ix) FEATURE:
             (A) NAME/KEY: HUMAN iNOS (781-792)
     1118
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
     1119
     1120
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
     1121
             (D) OTHER INFORMATION:
     1122
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:
     1123
     1124
            ProAlaLeuValGlnGlyIleLeuGluArgValVal
     1125
            510
     1126
     1127
     1128
                 (2) INFORMATION FOR SEQ ID NO: 60:
     1129
            (i) SEQUENCE CHARACTERISTICS:
     1130
             (A) LENGTH: 9
     1131
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR
     1132
            (ii) MOLECULE TYPE: PEPTIDE
     1133
            (ix) FEATURE:
     1134
             (A) NAME/KEY: HUMAN iNOS (781-789)
     1135
     1136
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
     1137
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
     1138
             (D) OTHER INFORMATION:
     1139
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:
     1140
     1141
            ProAlaLeuValGlnGlyIleLeuGlu
     1142
     1143
     1144
     1145
                 (2) INFORMATION FOR SEQ ID NO: 61:
     1146
            (i) SEQUENCE CHARACTERISTICS:
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1148
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR
1149
       (ii) MOLECULE TYPE: PEPTIDE
1150
1151
       (ix) FEATURE:
                                                                     Same
1152
        (A) NAME/KEY: HUMAN iNOS (781-786)
1153
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1154
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1155
        (D) OTHER INFORMATION:
1156
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:
1157
1158
       ProAlaLeuValGlnGly
1159
1160
1161
1162
            (2) INFORMATION FOR SEQ ID NO: 62:
1163
       (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18
1164
        (B) TYPE: AMINO ACID
1165
1166
        (D) TOPOLOGY: LINEAR
       (ii) MOLECULE TYPE: PEPTIDE
1167
       (ix) FEATURE:
1168
              (A) NAME/KEY: (G11) LOCUS HUMAN INOS (985-1002)
1169
              (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1170
              (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1171
              (D) OTHER INFORMATION:
1172
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:
1173
1174
       GlyIleValProPheArgSerPheTrpGlnGlnArgLeu
1175
1176
1177
       HisAspSerGlnHis
1178
1179
1180
1181
            (2) INFORMATION FOR SEQ ID NO: 63:
1182
       (i) SEQUENCE CHARACTERISTICS:
1183
        (A) LENGTH: 18
1184
        (B) TYPE: AMINO ACID
1185
        (D) TOPOLOGY: LINEAR
       (ii) MOLECULE TYPE: PEPTIDE
1186
1187
       (ix) FEATURE:
1188
        (A) NAME/KEY: HUMAN nNOS (1256-1273)
1189
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1190
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1191
        (D) OTHER INFORMATION:
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:
1192
1193
1194
       GlyIleAlaProPheArgSerPheTrpGlnGlnArgGln
1195
       510
1196
       PheAspIleGlnHis
1197
       15
1198
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	1199	
	1200	(2) INFORMATION FOR SEQ ID NO: 64:
	1201	(i) SEQUENCE CHARACTERISTICS:
>	1202	
	1203	(A) LENGTH: 15 (B) TYPE: AMINO ACID (D) TOPOLOGY: LINEAR (ii) MOLECULE TYPE: PEPTIDE
	1204	(D) TOPOLOGY: LINEAR
	1205	(ii) MOLECULE TYPE: PEPTIDE
	1206	(ix) FEATURE:
	1207	(A) NAME/KEY: HUMAN eNOS (1017-1031)
	1207	(B) LOCATION: CARBOXY TERMINAL WITH AMIDE
	1200	(C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
	1210	(D) OTHER INFORMATION:
	1211	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:
	1211	(XI) SEQUENCE DESCRIPTION: SEQ ID NO. 04.
		Glastical characteristics and approximation of the state
>	1213	GlyIleAlaProPheArgGlyPheTrpGlnGluArgLeu
_	1214	510
>	1215	HisAsp
	1216	15
	1217	
	1218	
	1219	(2) INFORMATION FOR SEQ ID NO: 65:
	1220	(i) SEQUENCE CHARACTERISTICS:
>	1221	(A) LENGTH: 15
	1222	(B) TYPE: AMINO ACID
	1223	(D) TOPOLOGY: LINEAR
	1224	(ii) MOLECULE TYPE: PEPTIDE
	1225	(ix) FEATURE:
	1226	(A) NAME/KEY: HUMAN iNOS (988-1002)
	1227	(B) LOCATION: CARBOXY TERMINAL WITH AMIDE
	1228	(C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
	1229	(D) OTHER INFORMATION:
	1230	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:
	1231	
>	1232	ProPheArgSerPheTrpGlnGlnArgLeuHisAspSer
•	1233	510
>	1234	GlnHis
-	1235	15
	1236	1
	1237	
	1238	(2) INFORMATION FOR SEQ ID NO: 66:
_	1239	(i) SEQUENCE CHARACTERISTICS:
>	1240	(A) LENGTH: 12
	1241	(B) TYPE: AMINO ACID
	1242	(D) TOPOLOGY: LINEAR
	1243	(ii) MOLECULE TYPE: PEPTIDE
	1244	(ix) FEATURE:
	1245	(A) NAME/KEY: HUMAN iNOS (991-1002)
	1246	(B) LOCATION: CARBOXY TERMINAL WITH AMIDE
	1247	(C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
	1248	(D) OTHER INFORMATION:

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			INPUT SET: S31225.raw
	1249	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:	
	1250		Sand
>	1251	SerPheTrpGlnGlnArgLeuHisAspSerGlnHis	1,10
	1252	510	
	1253		
	1254		
	1255	(2) INFORMATION FOR SEQ ID NO: 67:	ļ.
_	1256	(i) SEQUENCE CHARACTERISTICS:	
>	1257 1258	(A) LENGTH: 9	
		(B) TYPE: AMINO ACID (D) TOPOLOGY: LINEAR	
	1260	(ii) MOLECULE TYPE: PEPTIDE	
	1261	(ix) FEATURE:	
	1262	(A) NAME/KEY: HUMAN iNOS (994-1002)	
		(B) LOCATION: CARBOXY TERMINAL WITH AMIDE	
		(C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS	
	1265	(D) OTHER INFORMATION:	1
•	1266	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:	
	1267		
>	1268	GlnGlnArgLeuHisAspSerGlnHis	
	1269	5	
	1270		
	1271		İ
	1272	(2) INFORMATION FOR SEQ ID NO: 68:	
	1272	(2) INFORMATION FOR SEQ ID NO: 68: (i) SEQUENCE CHARACTERISTICS:	
>	1273	(A) LENGTH: 5	
	1275	(B) TYPE: AMINO ACID	İ
	1276	(D) TOPOLOGY: LINEAR	
	1277	(ii) MOLECULE TYPE: PEPTIDE	
	1278	(ix) FEATURE:	Ī
•	1279	(A) NAME/KEY: HUMAN iNOS (997-1002)	
	1280	(B) LOCATION: CARBOXY TERMINAL WITH AMIDE	
	1281	(C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS	
	1282	(D) OTHER INFORMATION:	
	1283	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:	
	1284		
>	1285	HisAspSerGlnHis	
	1286	5	· .
	1287		
	1288		1,
	1289	(2) INFORMATION FOR SEQ ID NO: 69:	
	1290	(i) SEQUENCE CHARACTERISTICS:	~
>	1291	(A) LENGTH: 15	
	1292	(B) TYPE: AMINO ACID	
	1293	(D) TOPOLOGY: LINEAR	
	1294	(ii) MOLECULE TYPE: PEPTIDE	
	1295	(ix) FEATURE:	
	1296	(A) NAME/KEY: HUMAN INOS (985-998)	
	1297	(B) LOCATION: CARBOXY TERMINAL WITH AMIDE	
	1298	(C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS	

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INPUT SET: S31225.raw 1299 (D) OTHER INFORMATION: Dane 1300 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69: 1301 1302 GlyIleValProPheArgSerPheTrpGlnGlnArgLeu 1303 510 1304 HisAsp 1305 15 1306 1307 1308 (2) INFORMATION FOR SEQ ID NO: 70: 1309 (i) SEQUENCE CHARACTERISTICS: 1310 (A) LENGTH: 12 1311 (B) TYPE: AMINO ACID 1312 (D) TOPOLOGY: LINEAR 1313 (ii) MOLECULE TYPE: PEPTIDE (ix) FEATURE: (A) NAME/KEY: HUMAN iNOS (985-996) 1315 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE 1316 1317 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS 1318 (D) OTHER INFORMATION: 1319 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70: 1320 1321 GlyIleValProPheArgSerPheTrpGlnGlnArg 1322 510 1323 1324 1325 (2) INFORMATION FOR SEQ ID NO: 71: 1326 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 9 1327 (B) TYPE: AMINO ACID 1328 (D) TOPOLOGY: LINEAR 1329 (ii) MOLECULE TYPE: PEPTIDE 1330 (ix) FEATURE: 1331 1332 (A) NAME/KEY: HUMAN iNOS (985-993) (B) LOCATION: CARBOXY TERMINAL WITH AMIDE 1333 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS 1334 1335 (D) OTHER INFORMATION: 1336 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71: 1337 1338 GlyIleValProPheArgSerPheTrp 1339 1340 1341 1342 (2) INFORMATION FOR SEQ ID NO: 72: 1343 (i) SEQUENCE CHARACTERISTICS: 1344 (A) LENGTH: 6 1345 (B) TYPE: AMINO ACID 1346 (D) TOPOLOGY: LINEAR 1347 (ii) MOLECULE TYPE: PEPTIDE 1348 (ix) FEATURE:

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INPUT SET: S31225.raw Same (A) NAME/KEY: HUMAN INOS (985-990) 1349 1350 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS 1351 1352 (D) OTHER INFORMATION: (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72: 1353 1354 1355 GlyIleValProPheArg 1356 1357 1358 1359 (2) INFORMATION FOR SEQ ID NO: 73: (i) SEQUENCE CHARACTERISTICS: 1360 (A) LENGTH: 18 1361 1362 (B) TYPE: AMINO ACID (D) TOPOLOGY: LINEAR 1363 (ii) MOLECULE TYPE: PEPTIDE 1364 1365 (ix) FEATURE: (A) NAME/KEY: (H1) LOCUS HUMAN INOS (1009-1026) 1366 1367 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS 1368 1369 (D) OTHER INFORMATION: (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73: 1370 1371 ${\tt ArgMetThrLeuValPheGlySerArgArgProAspGlu}$ 1372 510 1373 1374 AspHisIleTyrGln 1375 15 1376 . 1377 (2) INFORMATION FOR SEQ ID NO: 74: 1378 1379 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 1380 1381 (B) TYPE: AMINO ACID (D) TOPOLOGY: LINEAR 1382 (ii) MOLECULE TYPE: PEPTIDE 1383 (ix) FEATURE: 1384 1385 (A) NAME/KEY: HUMAN eNOS (1041-1057) (B) LOCATION: CARBOXY TERMINAL WITH AMIDE 1386 1387 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS 1388 (D) OTHER INFORMATION: (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74: 1389 1390 1391 MetThrLeuValPheGlySerArgSerSerGlnLeuAsp 1392 510 HisLeuTyrArg 1393 1394 15 1395

1396

^{1397 (2)} INFORMATION FOR SEQ ID NO: 75:

^{1398 (}i) SEQUENCE CHARACTERISTICS:

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1399
             (A) LENGTH: 17
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             (B) TYPE: AMINO ACID
     1400
     1401
             (D) TOPOLOGY: LINEAR
     1402
            (ii) MOLECULE TYPE: PEPTIDE
                                                                   Same
     1403
            (ix) FEATURE:
     1404
             (A) NAME/KEY: HUMAN nNOS (1281-1297)
     1405
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
     1406
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
     1407
             (D) OTHER INFORMATION:
     1408
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:
     1409
     1410
            MetValLeuValPheGlySerArgGlnSerLysIleAsp
     1411
            510
     1412
            HisIleTyrArg
     1413
            15
     1414
     1415
     1416
                 (2) INFORMATION FOR SEQ ID NO: 76:
     1417
            (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 15
     1418
     1419
             (B) TYPE: AMINO ACID
     1420
             (D) TOPOLOGY: LINEAR
            (ii) MOLECULE TYPE: PEPTIDE
     1421
            (ix) FEATURE:
     1422
             (A) NAME/KEY: HUMAN iNOS (1012-1026)
     1423
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
     1424
     1425
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
     1426
             (D) OTHER INFORMATION:
     1427
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:
     1428
     1429
            LeuValPheClySerArgArgProAspGluAspHisIle
     1430
            510
-->
     1431
            TyrGln
     1432
     1433
     1434
     1435
                 (2) INFORMATION FOR SEQ ID NO: 77:
     1436
            (i) SEQUENCE CHARACTERISTICS:
     1437
             (A) LENGTH: 12
     1438
             (B) TYPE: AMINO ACID
     1439
             (D) TOPOLOGY: LINEAR
     1440
            (ii) MOLECULE TYPE: PEPTIDE
     1441
            (ix) FEATURE:
             (A) NAME/KEY: HUMAN iNOS (1015-1026)
     1442
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
     1443
     1444
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
     1445
             (D) OTHER INFORMATION:
     1446
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:
     1447
     1448
            GlySerArgArgProAspGluAspHisIleTyrGln
     1449
            510
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/833,506A

DATE: 03/29/1999 TIME: 08:48:19

1451 1452 1453 1454 (2) INFORMATION FOR SEQ ID NO: 78: 1455 (A) LENCTH: 9 1457 (B) TYPE: AMINO ACID 1458 (D) TOPOLOGY: LINEAR 1459 (I) MOLECULE TYPE: PEPTIDE 1460 (IX) FEATURE: 1461 (A) NAME/KEY: HUMAN INOS (1018-1026) 1462 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE 1463 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS 1464 (D) OTHER INFORMATION: 1465 (X) SEQUENCE DESCRIPTION: SEQ ID NO: 78: 1466 (X) SEQUENCE CHARACTERISTICS: -> 1467 ArgProaspGluAspHislleTyrGln 1470 1471 (2) INFORMATION FOR SEQ ID NO: 79: 1472 (A) LENCTH: 6 1474 (B) TYPE: AMINO ACID 1475 (I) MOLECULE TYPE: PEPTIDE 1476 (I) MOLECULE TYPE: PEPTIDE 1477 (IX) FEATURE: 1478 (A) NAME/KEY: HUMAN INOS (1021-1026) 1480 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS 1481 (D) OTHER INFORMATION: SEQ ID NO: 79: 1482 (X) SEQUENCE DESCRIPTION: SEQ ID NO: 79: 1483 1481 (D) OTHER INFORMATION: 1482 (X) SEQUENCE DESCRIPTION: SEQ ID NO: 79: 1484 (G) HARD SEQUENCE DESCRIPTION: SEQ ID NO: 79: 1485 1486 1487 1488 (2) INFORMATION FOR SEQ ID NO: 80: 1489 (1) SEQUENCE CHARACTERISTICS:> 1490 (A) LENCTH: 15 1491 (B) TYPE: AMINO ACID 1492 (I) SEQUENCE CHARACTERISTICS:> 1490 (A) LENCTH: 15 1491 (E) DIPPIC AMINO ACID 1492 (I) SEQUENCE CHARACTERISTICS:> 1490 (A) LENCTH: 15 1491 (E) DIPPIC AMINO ACID 1492 (I) SEQUENCE CHARACTERISTICS:> 1490 (A) LENCTH: 15 1491 (E) DIPPIC AMINO ACID 1492 (I) SEQUENCE CHARACTERISTICS:> 1490 (A) LENCTH: 15 1491 (E) DIPPIC AMINO ACID 1492 (I) SEQUENCE CHARACTERISTICS:> 1490 (A) LENCTH: 15 1491 (A) NAME/KEY: HUMAN INOS (1009-1023) 1496 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE 1497 (C) LIDENTIFICATION METHOD: AMINO ACID AMALYSIS				INPUT SET: S31225.raw
1452 1453 1454 (2) INFORMATION FOR SEQ ID NO: 78: 1455 (i) SEQUENCE CHARACTERISTICS:> 1456 (A) LENGTH: 9 1457 (B) Type: AMINO ACID 1458 (D) TOPOLOGY: LINEAR 1459 (ii) MOLECULE TYPE: PEPTIDE 1460 (ix) FEATURE: 1461 (A) NAME/KEY: HUMAN INOS (1018-1026) 1462 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE 1463 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS 1464 (D) OTHER INFORMATION: SEQ ID NO: 78: 1465 (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 78: 1466 (x) SEQUENCE CHARACTERISTICS:> 1467 ArgproAspGluAspBislleTyrGln 1470 1471 (2) INFORMATION FOR SEQ ID NO: 79: 1472 (3) SEQUENCE CHARACTERISTICS:> 1473 (A) LENGTH: 6 1474 (B) TYPE: AMINO ACID 1475 (ii) MOLECULE TYPE: PEPTIDE 1476 (ii) MOLECULE TYPE: PEPTIDE 1477 (ix) FEATURE: 1478 (A) NAME/KEY: HUMAN INOS (1021-1026) 1479 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE 1480 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS 1481 (D) OTHER INFORMATION: 1482 (XI) SEQUENCE DESCRIPTION: SEQ ID NO: 79: 1483> 1484 (C) LENGTH: 15 1485 (S) LOCATION: CARBOXY TERMINAL WITH AMIDE 1489 (i) SEQUENCE CHARACTERISTICS:> 1490 (A) LENGTH: 15 1491 (B) TYPE: AMINO ACID 1492 (D) TOPOLOGY: LINEAR 1493 (ii) MOLECULE TYPE: PEPTIDE 1494 (X) FEATURE: 1495 (A) NAME/KEY: HUMAN INOS (1009-1023) 1495 (A) NAME/KEY: HUMAN INOS (1009-1023) 1496 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE		1450		
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1478 (A) NAME/KEY: HUMAN INOS (1021-1026) 1479 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE 1480 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS 1481 (D) OTHER INFORMATION: 1482 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79: 1483> 1484 GluAspHislleTyrGln 1485 5 1486 1487 1488 (2) INFORMATION FOR SEQ ID NO: 80: 1489 (i) SEQUENCE CHARACTERISTICS:> 1490 (A) LENGTH: 15 1491 (B) TYPE: AMINO ACID 1492 (D) TOPOLOGY: LINEAR 1493 (ii) MOLECULE TYPE: PEPTIDE 1494 (ix) FEATURE: 1495 (A) NAME/KEY: HUMAN INOS (1009-1023) 1496 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE			, ,	
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1491 (B) TYPE: AMINO ACID 1492 (D) TOPOLOGY: LINEAR 1493 (ii) MOLECULE TYPE: PEPTIDE 1494 (ix) FEATURE: 1495 (A) NAME/KEY: HUMAN INOS (1009-1023) 1496 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE				
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1494 (ix) FEATURE: 1495 (A) NAME/KEY: HUMAN iNOS (1009-1023) 1496 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE			·	U/
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1496 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE			· ·	
, ,			(A) NAME/KEY! MUMAN INOS (1009-1023)	
145/ (C) IDENTIFICATION METROD: AMINO ACID ANALYSIS				
·		1496	(B) LOCATION: CARBOXY TERMINAL WITH AMIDE	
· ·		1496 1497	(B) LOCATION: CARBOXY TERMINAL WITH AMIDE (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS	
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/833,506A

DATE: 03/29/1999 TIME: 08:48:19

		INPUT SET: S31225.raw
	1500	
>	1501	ArgMetThrLeuValPheGlySerArgArgProAspGlu
	1502	510
>	1503	AspHis
*	1504	15
	1505	510 AspHis 15
	1506	
	1300	
	1507	(2) INFORMATION FOR SEQ ID NO: 81:
	1508	(i) SEQUENCE CHARACTERISTICS:
>	1509	(A) LENGTH: 11
	1510	(B) TYPE: AMINO ACID
	1511	(D) TOPOLOGY: LINEAR
	1512	(ii) MOLECULE TYPE: PEPTIDE
	1512	(ix) FEATURE:
	1514	(A) NAME/KEY: HUMAN INOS (1009-1020)
	1514	
		(B) LOCATION: CARBOXY TERMINAL WITH AMIDE
	1516	(C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
	1517	(D) OTHER INFORMATION:
	1518	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:
	1519	
>	1520	ArgMetThrLeuValPheGlySerArgArgPro
	1521	510
	1522	· · · · · · · · · · · · · · · · · · ·
	1523	
	1504	(A) TWEEDWATTON FOR GEO TO NO. 00.
	1524	(2) INFORMATION FOR SEQ ID NO: 82:
_	1525	(i) SEQUENCE CHARACTERISTICS:
>	1526	(A) LENGTH: 9
	1527	(B) TYPE: AMINO ACID
	1528	(D) TOPOLOGY: LINEAR
	1529	(ii) MOLECULE TYPE: PEPTIDE
	1530	(ix) FEATURE:
	1531	(A) NAME/KEY: HUMAN iNOS (1009-1017)
	1532	(B) LOCATION: CARBOXY TERMINAL WITH AMIDE
	1533	(C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
	1534	(D) OTHER INFORMATION:
	1535	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:
_	1536	(B) LOCATION: CARBOXY TERMINAL WITH AMIDE (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS (D) OTHER INFORMATION: (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82: ArgMetThrLeuValPheGlySerArg-amide 5
>	1537	ArgMetThrLeuValPheGlySerArg-amide
	1538	5 minerical minerical services
	1539	The state of the s
	1540	Mark Jan 1
	1543	(A) TYPODYARTON FOR CEO TR NO. 02.
	1541	(2) INFORMATION FOR SEQ ID NO: 83:
_	1542	(i) SEQUENCE CHARACTERISTICS:
>	1543	(A) LENGTH: 6
	1544	(B) TYPE: AMINO ACID
	1545	(D) TOPOLOGY: LINEAR
	1546	(ii) MOLECULE TYPE: PEPTIDE
	1547	(ix) FEATURE:
	1548	(A) NAME/KEY: HUMAN iNOS (1009-1014)
	1549	(B) LOCATION: CARBOXY TERMINAL WITH AMIDE

RAW SEQUENCE LISTING PATENT APPLICATION US/08/833,506A

DATE: 03/29/1999 TIME: 08:48:20

			INPUT SET: S31225.raw
	1550	(C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS	
	1551	(D) OTHER INFORMATION:	•
	1552	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:	
	1553		~
>	1554	ArgMetThrLeuValPhe(-amide)	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
	1555	5	· · · · · · · · · · · · · · · · · · ·
	1556	· 1	ane (11)
	1557		W . M
	1558		
	1550	(2) INFORMATION FOR SEQ ID NO: 84:	sine TAB
	1559 1560	(i) SEQUENCE CHARACTERISTICS:	
>	1561	(A) LENGTH: 12	
	1562	(B) TYPE: AMINO ACID	
	1563	(D) TOPOLOGY: LINEAR	
	1564	(ii) MOLECULE TYPE: PEPTIDE	
	1565	(ix) FEATURE:	
	1566	(A) NAME/KEY: TRUNCATED HUMAN INOS (40-54)	
	1567	(B) LOCATION: CARBOXY TERMINAL WITH AMIDE	
	1568	(C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS	
	1569	(D) OTHER INFORMATION:	
	1570	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:	
	1571	, , _	
>	1572	ThrGlnAspAspLeuGlnTyrHisAsnLeuSerLys	i .
	1573	510	
	1574		
	1575		
			, , , , , , , , , , , , , , , , , , ,
	1576	(2) INFORMATION FOR SEQ ID NO: 85:	
	1577	(i) SEQUENCE CHARACTERISTICS:	1
>	1 578 1579	(A) LENGTH: 9 (B) TYPE: AMINO ACID	
	1580	(D) TOPOLOGY: LINEAR	
	1581	(ii) MOLECULE TYPE: PEPTIDE	
	1582	(ix) FEATURE:	
	1583	(A) NAME/KEY: TRUNCATED HUMAN INOS (784-798)	
	1584	(B) LOCATION: CARBOXY TERMINAL WITH AMIDE	1
	1585	(C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS	
	1586	(D) OTHER INFORMATION:	
	1587	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:	
	1588		
>	1589	ValGlnGlyIleLeuGluArgValVal	1
	1590	5	1
	1591		1,
	1592		1/
	1502	(2) INFORMATION FOR CEO ID NO. 06.	<u> </u>
	1593	(2) INFORMATION FOR SEQ ID NO: 86:	
	1594 1595	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18	
/	1596	(B) TYPE: AMINO ACID	
	1597	(D) TOPOLOGY: LINEAR	
	1598	(ii) MOLECULE TYPE: PEPTIDE	
	1599	(ix) FEATURE:	
		/ === / = ==== = :	

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INPUT SET: S31225.raw

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1600
        (A) NAME/KEY: HUMAN iNOS (37-54)
1601
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1602
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1603
        (D) OTHER INFORMATION:
                                                              same
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:
1604
1605
1606
      SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
1607
      510
1608
      SerLysGlnGlnAsn
1609
      15
1610
1611
            (2) INFORMATION FOR SEQ ID NO: 87:
1612
       (i) SEQUENCE CHARACTERISTICS:
1613
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1615
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR
1616
       (ii) MOLECULE TYPE: PEPTIDE
1617
1618
       (ix) FEATURE:
        (A) NAME/KEY: HUMAN INOS (41-45)
1619
1620
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1621
1622
        (D) OTHER INFORMATION:
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:
1623
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1625
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1628
1629
            (2) INFORMATION FOR SEQ ID NO: 88:
1630
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1631
        (A) LENGTH: 6
1632
        (B) TYPE: AMINO ACID
1633
        (D) TOPOLOGY: LINEAR
       (ii) MOLECULE TYPE: PEPTIDE
1634
1635
       (ix) FEATURE:
1636
        (A) NAME/KEY: HUMAN iNOS (40-45)
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1637
1638
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1639
        (D) OTHER INFORMATION:
1640
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:
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1643
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1646
            (2) INFORMATION FOR SEQ ID NO: 89:
1647
       (i) SEQUENCE CHARACTERISTICS:
1648
        (A) LENGTH: 7
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(B) TYPE: AMINO ACID

1649

1699

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1650
       (D) TOPOLOGY: LINEAR
1651
       (ii) MOLECULE TYPE: PEPTIDE
1652
       (ix) FEATURE:
1653
        (A) NAME/KEY: HUMAN INOS (39-45)
1654
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
                                                               Sur
1655
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1656
       (D) OTHER INFORMATION:
1657
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:
1658
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1659
1660
      5
1661
1662
1663
1664
            (2) INFORMATION FOR SEQ ID NO: 90:
1665
1666
       (i) SEQUENCE CHARACTERISTICS:
1667
       (A) LENGTH: 8
1668
       (B) TYPE: AMINO ACID
       (D) TOPOLOGY: LINEAR
1669
       (ii) MOLECULE TYPE: PEPTIDE
1670
      (ix) FEATURE:
1671
       (A) NAME/KEY: HUMAN iNOS (38-45)
1672
       (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1673
       (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1674
1675
       (D) OTHER INFORMATION:
1676
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:
1677
1678
      ProValThrGlnAspAspLeuGln
1679
1680
1681
1682
            (2) INFORMATION FOR SEQ ID NO: 91:
1683
      (i) SEQUENCE CHARACTERISTICS:
1684
       (A) LENGTH: 9
1685
       (B) TYPE: AMINO ACID
1686
       (D) TOPOLOGY: LINEAR
       (ii) MOLECULE TYPE: PEPTIDE
1687
1688
      (ix) FEATURE:
1689
       (A) NAME/KEY: HUMAN INOS (37-45)
       (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1690
       (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1691
1692
       (D) OTHER INFORMATION:
1693
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:
1694
1695
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1696
1697
1698
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1700
       (i) SEQUENCE CHARACTERISTICS:
1701
        (A) LENGTH: 5
1702
        (B) TYPE: AMINO ACID
1703
        (D) TOPOLOGY: LINEAR
       (ii) MOLECULE TYPE: PEPTIDE
1704
1705
       (ix) FEATURE:
        (A) NAME/KEY: HUMAN iNOS (40-44)
1706
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1707
1708
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1709
        (D) OTHER INFORMATION:
1710
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:
1711
1712
      ThrGlnAspAspLeu
1713
1714
1715
1716
1717
            (2) INFORMATION FOR SEQ ID NO: 93:
1718
       (i) SEQUENCE CHARACTERISTICS:
1719
        (A) LENGTH: 6
        (B) TYPE: AMINO ACID
1720
        (D) TOPOLOGY: LINEAR
1721
       (ii) MOLECULE TYPE: PEPTIDE
1722
1723
      (ix) FEATURE:
        (A) NAME/KEY: HUMAN iNOS (39-44)
1724
1725
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1726
1727
        (D) OTHER INFORMATION:
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:
1728
1729
1730
      ValThrGlnAspAspLeu
1731
1732
1733
1734 .
            (2) INFORMATION FOR SEQ ID NO: 94:
1735
       (i) SEQUENCE CHARACTERISTICS:
1736
        (A) LENGTH: 7
1737
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR
1738
       (ii) MOLECULE TYPE: PEPTIDE
1739
1740
      (ix) FEATURE:
        (A) NAME/KEY: HUMAN iNOS (38-44)
1741
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1742
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1743
1744
        (D) OTHER INFORMATION:
1745
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:
1746
1747
      ProValThrGlnAspAspLeu
1748
1749
1750
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1751
            (2) INFORMATION FOR SEQ ID NO: 95:
1752
       (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 8
1753
        (B) TYPE: AMINO ACID
1754
1755
        (D) TOPOLOGY: LINEAR
       (ii) MOLECULE TYPE: PEPTIDE
1756
1757
       (ix) FEATURE:
        (A) NAME/KEY: HUMAN iNOS (37-44)
1758
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1759
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1760
        (D) OTHER INFORMATION:
1761
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:
1762
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1764
1765
1766
1767
1768
1769
            (2) INFORMATION FOR SEQ ID NO: 96:
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1770
        (A) LENGTH: 9
1771
        (B) TYPE: AMINO ACID
1772
1773
        (D) TOPOLOGY: LINEAR
1774
       (ii) MOLECULE TYPE: PEPTIDE
1775
       (ix) FEATURE:
        (A) NAME/KEY: HUMAN iNOS (36-44)
1776
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1777
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1778
        (D) OTHER INFORMATION:
1779
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:
1780
1781
1782
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1783
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1785
           (2) INFORMATION FOR SEQ ID NO: 97:
1786
1787
       (i) SEQUENCE CHARACTERISTICS:
1788
        (A) LENGTH: 5
1789
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR
1790
       (ii) MOLECULE TYPE: PEPTIDE
1791
1792
       (ix) FEATURE:
        (A) NAME/KEY: HUMAN iNOS (39-43)
1793
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1794
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1796
        (D) OTHER INFORMATION:
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:
1797
1798
1799
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1800
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1802
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1804
       (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 6
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                                                            sone
1806
        (B) TYPE: AMINO ACID
1807
        (D) TOPOLOGY: LINEAR
1808
       (ii) MOLECULE TYPE: PEPTIDE
1809
       (ix) FEATURE:
        (A) NAME/KEY: HUMAN iNOS (38-43)
1810
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
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1812
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1813
        (D) OTHER INFORMATION:
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:
1814
1815
1816
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1817
1818
1819
1820
1821
            (2) INFORMATION FOR SEQ ID NO: 99:
       (i) SEQUENCE CHARACTERISTICS:
1822
        (A) LENGTH: 7
1823
        (B) TYPE: AMINO ACID
1824
1825
        (D) TOPOLOGY: LINEAR
1826
       (ii) MOLECULE TYPE: PEPTIDE
       (ix) FEATURE:
1827
1828
        (A) NAME/KEY: HUMAN INOS (37-43)
1829
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1830
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1831
        (D) OTHER INFORMATION:
1832
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:
1833
1834
      SerProValThrGlnAspAsp
1835
1836
1837
1838
            (2) INFORMATION FOR SEQ ID NO: 100:
1839
       (i) SEQUENCE CHARACTERISTICS:
1840
        (A) LENGTH: 8
1841
        (B) TYPE: AMINO ACID
1842
        (D) TOPOLOGY: LINEAR
1843
       (ii) MOLECULE TYPE: PEPTIDE
1844
       (ix) FEATURE:
        (A) NAME/KEY: HUMAN iNOS (36-43)
1845
1846
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1847
1848
        (D) OTHER INFORMATION:
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:
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1850
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SerSerProValThrGlnAspAsp
1851
                                                                  same
1852
1853
1854
1855
            (2) INFORMATION FOR SEQ ID NO: 101:
1856
       (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 9
1857
        (B) TYPE: AMINO ACID
1858
1859
        (D) TOPOLOGY: LINEAR
1860
       (ii) MOLECULE TYPE: PEPTIDE
1861
       (ix) FEATURE:
        (A) NAME/KEY: HUMAN INOS (35-43)
1862
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1863
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1864
        (D) OTHER INFORMATION:
1865
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:
1866
1867
1868
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1869
1870
1871
1872
1873
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1874
       (i) SEQUENCE CHARACTERISTICS:
1875
        (A) LENGTH: 18
        (B) TYPE: AMINO ACID
1876
        (D) TOPOLOGY: LINEAR
1877
       (ii) MOLECULE TYPE: PEPTIDE
1878
       (ix) FEATURE:
1879
        (A) NAME/KEY: HUMAN iNOS (37-54)
1880
1881
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1882
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
        (D) OTHER INFORMATION:
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1884
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:
1885
1886
      SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
1887
      510
1888
      SerLysGlnGlnAsn
1889
1890
1891
            (2) INFORMATION FOR SEQ ID NO: 103:
1892
1893
       (i) SEQUENCE CHARACTERISTICS:
1894
        (A) LENGTH: 15
1895
        (B) TYPE: AMINO ACID
1896
        (D) TOPOLOGY: LINEAR
1897
       (ii) MOLECULE TYPE: PEPTIDE
1898
       (ix) FEATURE:
1899
        (A) NAME/KEY: HUMAN INOS (40-54)
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1900
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        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1902
        (D) OTHER INFORMATION:
1903
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:
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1904
1905
      ThrGlnAspAspLeuGlnTyrHisAsnLeuSerLysGln
1906
1907
      GlnAsn
1908
      15
1909
1910
1911
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1913
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1914
        (B) TYPE: AMINO ACID
1915
        (D) TOPOLOGY: LINEAR
       (ii) MOLECULE TYPE: PEPTIDE
1916
1917
      (ix) FEATURE:
1918
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1919
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1920
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
        (D) OTHER INFORMATION:
1921
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:
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1923
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1926
      510
1927
1928
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1929
       (i) SEQUENCE CHARACTERISTICS:
1930
1931
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1932
        (B) TYPE: AMINO ACID
1933
        (D) TOPOLOGY: LINEAR
       (ii) MOLECULE TYPE: PEPTIDE
1934
1935
      (ix) FEATURE:
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1936
1937
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1938
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1939
        (D) OTHER INFORMATION:
1940
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1941
1942
      TyrHisAsnLeuSerLysGlnGlnAsn
1943
1944
1945
1946
            (2) INFORMATION FOR SEQ ID NO: 106:
1947
       (i) SEQUENCE CHARACTERISTICS:
1948
        (A) LENGTH: 6
1949
        (B) TYPE: AMINO ACID
1950
        (D) TOPOLOGY: LINEAR
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2000

(i) SEQUENCE CHARACTERISTICS:

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1951
       (ii) MOLECULE TYPE: PEPTIDE
1952
       (ix) FEATURE:
1953
        (A) NAME/KEY: HUMAN iNOS (49-54)
                                                                sane
1954
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1955
1956
        (D) OTHER INFORMATION:
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:
1957
1958
1959
      LeuSerLysGlnGlnAsn
1960
1961
1962
1963
            (2) INFORMATION FOR SEQ ID NO: 107:
       (i) SEQUENCE CHARACTERISTICS:
1964
1965
        (A) LENGTH: 15
1966
        (B) TYPE: AMINO ACID
1967
        (D) TOPOLOGY: LINEAR
1968
       (ii) MOLECULE TYPE: PEPTIDE
1969
      (ix) FEATURE:
1970
        (A) NAME/KEY: HUMAN iNOS (37-51)
1971
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1972
1973
        (D) OTHER INFORMATION:
1974
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:
1975
1976
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1977
      510
1978
      SerLys
1979
      15
1980
1981
            (2) INFORMATION FOR SEQ ID NO: 108:
1982
1983
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1984
        (A) LENGTH: 12
1985
        (B) TYPE: AMINO ACID
1986
        (D) TOPOLOGY: LINEAR
      (ii) MOLECULE TYPE: PEPTIDE
1987
1988
      (ix) FEATURE:
1989
        (A) NAME/KEY: HUMAN iNOS (37-48)
1990
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1991
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1992
        (D) OTHER INFORMATION:
1993
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:
1994
1995
      SerProValThrGlnAspAspLeuGlnTyrHisAsn
1996
      510
1997
1998
1999
            (2) INFORMATION FOR SEO ID NO: 109:
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2051

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             (B) TYPE: AMINO ACID
     2002
     2003
             (D) TOPOLOGY: LINEAR
     2004
            (ii) MOLECULE TYPE: PEPTIDE
     2005
            (ix) FEATURE:
                                                                     same
     2006
             (A) NAME/KEY: HUMAN iNOS (37-45)
     2007
            (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
     2008
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
             (D) OTHER INFORMATION:
     2009
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     2010
     2011
     2012
           SerProValThrGlnAspAspLeuGln
     2013
     2014
     2015
                 (2) INFORMATION FOR SEQ ID NO: 110:
     2016
            (i) SEQUENCE CHARACTERISTICS:
     2017
             (A) LENGTH: 6
     2018
     2019
             (B) TYPE: AMINO ACID
     2020
             (D) TOPOLOGY: LINEAR
            (ii) MOLECULE TYPE: PEPTIDE
     2021
            (ix) FEATURE:
     2022
             (A) NAME/KEY: HUMAN INOS (37-42)
     2023
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
     2024
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
     2025
     2026
             (D) OTHER INFORMATION:
     2027
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:
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     2029
     2030
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     2031
     2032
     2033
     2034
                 (2) INFORMATION FOR SEQ ID NO: 111:
     2035
            (i) SEQUENCE CHARACTERISTICS:
     2036
             (A) LENGTH: 10
     2037
             (B) TYPE: AMINO ACID
     2038
             (D) TOPOLOGY: LINEAR
     2039
            (ii) MOLECULE TYPE: PEPTIDE
     2040
            (ix) FEATURE:
             (A) NAME/KEY: HUMAN iNOS (35-44)
     2041
     2042
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
     2043
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
     2044
             (D) OTHER INFORMATION:
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     2046
     2047
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     2048
            510
     2049
     2050
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2103
2104
2105
            (2) INFORMATION FOR SEQ ID NO: 115:
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2106
                                                                Sand
2107
        (A) LENGTH: 7
2108
        (B) TYPE: AMINO ACID
2109
        (D) TOPOLOGY: LINEAR
       (ii) MOLECULE TYPE: PEPTIDE
2110
       (ix) FEATURE:
2111
        (A) NAME/KEY: HUMAN iNOS (786-792)
2112
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2113
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2114
2115
        (D) OTHER INFORMATION:
2116
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:
2117
2118
      GlyIleLeuGluArgValVal
2119
2120
2121
2122
            (2) INFORMATION FOR SEQ ID NO: 116:
2123
       (i) SEQUENCE CHARACTERISTICS:
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        (A) LENGTH: 8
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        (B) TYPE: AMINO ACID
2126
        (D) TOPOLOGY: LINEAR
2127
       (ii) MOLECULE TYPE: PEPTIDE
       (ix) FEATURE:
2128
        (A) NAME/KEY: HUMAN INOS (785-792)
2129
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2130
2131
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2132
        (D) OTHER INFORMATION:
2133
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:
2134
2135
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2136
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2138
2139
2140
            (2) INFORMATION FOR SEQ ID NO: 117:
       (i) SEQUENCE CHARACTERISTICS:
2141
2142
        (A) LENGTH: 9
2143
        (B) TYPE: AMINO ACID
2144
        (D) TOPOLOGY: LINEAR
2145
       (ii) MOLECULE TYPE: PEPTIDE
2146
      (ix) FEATURE:
2147
        (A) NAME/KEY: HUMAN iNOS (784-792)
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2148
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2149
2150
        (D) OTHER INFORMATION:
2151
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:
2152
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/833,506A

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2052
            (i) SEQUENCE CHARACTERISTICS:
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             (A) LENGTH: 18
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             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR
     2055
                                                                    some
            (ii) MOLECULE TYPE: PEPTIDE
     2056
            (ix) FEATURE:
     2057
             (A) NAME/KEY: HUMAN iNOS (781-798)
     2058
     2059
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
     2060
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
     2061
             (D) OTHER INFORMATION:
     2062
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:
     2063
--> 2064
           ProAlaLeuValGlnGlyIleLeuGluArgValValAsp
     2065
           510
    2066
           GlyProThrProHis
           15
     2067
     2068
     2069
     2070
                 (2) INFORMATION FOR SEQ ID NO: 113:
           (i) SEQUENCE CHARACTERISTICS:
     2071
     2072
             (A) LENGTH: 5
     2073
             (B) TYPE: AMINO ACID
     2074
             (D) TOPOLOGY: LINEAR
            (ii) MOLECULE TYPE: PEPTIDE
     2075
     2076
           (ix) FEATURE:
     2077
             (A) NAME/KEY: HUMAN iNOS (788-792)
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
     2078
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
     2079
     2080
            (D) OTHER INFORMATION:
     2081
     2082
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:
     2083
     2084
           LeuGluArgValVal
     2085
     2086
     2087
     2088
                (2) INFORMATION FOR SEQ ID NO: 114:
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           (i) SEQUENCE CHARACTERISTICS:
    2090
            (A) LENGTH: 6
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            (B) TYPE: AMINO ACID
     2092
            (D) TOPOLOGY: LINEAR
           (ii) MOLECULE TYPE: PEPTIDE
     2093
     2094
           (ix) FEATURE:
     2095
             (A) NAME/KEY: HUMAN iNOS (787-792)
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
     2096
            (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
     2097
     2098
            (D) OTHER INFORMATION:
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    2101
           IleLeuGluArgValVal
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/833,506A

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2153
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2154
2155
2156
2157
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       (i) SEQUENCE CHARACTERISTICS:
2158
        (A) LENGTH: 5
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        (D) TOPOLOGY: LINEAR
2162
       (ii) MOLECULE TYPE: PEPTIDE
2163
      (ix) FEATURE:
2164
        (A) NAME/KEY: HUMAN iNOS (787-791)
2165
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
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2167
        (D) OTHER INFORMATION:
2168
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2170
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2171
2172
2173
2174
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        (A) LENGTH: 6
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        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR
2178
      (ii) MOLECULE TYPE: PEPTIDE
2179
      (ix) FEATURE:
2180
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2181
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2182
2183
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2184
       (D) OTHER INFORMATION:
2185
2186
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2187
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2188
2189
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2191
2192
           (2) INFORMATION FOR SEQ ID NO: 120:
2193
      (i) SEQUENCE CHARACTERISTICS:
2194
        (A) LENGTH: 7
2195
        (B) TYPE: AMINO ACID
2196
        (D) TOPOLOGY: LINEAR
2197
      (ii) MOLECULE TYPE: PEPTIDE
2198
      (ix) FEATURE:
2199
        (A) NAME/KEY: HUMAN iNOS (785-791)
2200
        (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2201
        (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2202
       (D) OTHER INFORMATION:
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2203
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:
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     2205
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     2206
     2207
     2208
     2209
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             (A) LENGTH: 8
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             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR
     2213
            (ii) MOLECULE TYPE: PEPTIDE
     2214
     2215
            (ix) FEATURE:
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     2216
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
     2217
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
     2218
     2219
             (D) OTHER INFORMATION:
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     2223
     2224
     2225
     2226
                 (2) INFORMATION FOR SEQ ID NO: 122:
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            (i) SEQUENCE CHARACTERISTICS:
     2228
             (A) LENGTH: 9
             (B) TYPE: AMINO ACID
     2229
             (D) TOPOLOGY: LINEAR
     2230
            (ii) MOLECULE TYPE: PEPTIDE
     2231
     2232
            (ix) FEATURE:
     2233
             (A) NAME/KEY: HUMAN iNOS (783-791)
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
     2234
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
     2235
     2236
            (D) OTHER INFORMATION:
     2237
     2238
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     2240
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     2241
     2242
     2243
     2244
                 (2) INFORMATION FOR SEQ ID NO: 123:
     2245
            (i) SEQUENCE CHARACTERISTICS:
     2246
             (A) LENGTH: 5
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             (B) TYPE: AMINO ACID
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             (D) TOPOLOGY: LINEAR
     2249
            (ii) MOLECULE TYPE: PEPTIDE
     2250
            (ix) FEATURE:
             (A) NAME/KEY: HUMAN iNOS (786-790)
     2251
     2252
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
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(C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
     2253
     2254
             (D) OTHER INFORMATION:
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     2255
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:
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     2257
     2258
     2259
     2260
     2261
                 (2) INFORMATION FOR SEQ ID NO: 124:
     2262
            (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 6
     2263
     2264
             (B) TYPE: AMINO ACID
     2265
             (D) TOPOLOGY: LINEAR
            (ii) MOLECULE TYPE: PEPTIDE
     2266
     2267
            (ix) FEATURE:
             (A) NAME/KEY: HUMAN INOS (785-790)
     2268
     2269
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
     2270
     2271
            (D) OTHER INFORMATION:
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            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:
     2273
   2274
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     2275
     2276
     2277
     2278
                 (2) INFORMATION FOR SEQ ID NO: 125:
            (i) SEQUENCE CHARACTERISTICS:
     2279
             (A) LENGTH: 7
     2280
     2281
             (B) TYPE: AMINO ACID
     2282
             (D) TOPOLOGY: LINEAR
            (ii) MOLECULE TYPE: PEPTIDE
     2283
            (ix) FEATURE:
     2284
             (A) NAME/KEY: HUMAN INOS (784-790)
     2285
             (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
     2286
             (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
     2287
             (D) OTHER INFORMATION:
     2288
     2289
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:
     2290
     2291
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     2292
     2293
     2294
     2295
     2296
                (2) INFORMATION FOR SEQ ID NO: 126:
     2297
            (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 8
    2298
             (B) TYPE: AMINO ACID
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             (D) TOPOLOGY: LINEAR
     2300
     2301
            (ii) MOLECULE TYPE: PEPTIDE
     2302
            (ix) FEATURE:
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/833,506A

DATE: 03/29/1999 TIME: 08:48:25

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	2304	(B)	LOCATION: CARBOXY TERMINAL WITH AMIDE	same
	2305	(C)	IDENTIFICATION METHOD: AMINO ACID ANALYSIS	a A M
	2306	(D)	OTHER INFORMATION:	
	2307			
	2308	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 126:	
	2309			
>	2310	LeuVa	alGlnGlyIleLeuGluArg	
	2311	5_		
	2312	(J)	delete et end of file	
>	2313	(33)	I delle et ma)	
	2314		W	
	2315			
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	2320 2321			•
	2321			
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	2324			
	2326			
	2320			

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/833,506A

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20 Wrong application Serial Number 37 Entered (18) and Cale. Seq. Length (0) differ 58 Entered (18) and Cale. Seq. Length (0) differ 69 Wrong Amino Acid Designator 71 Wrong Amino Acid Designator 72 Entered (18) and Cale. Seq. Length (0) differ 88 Wrong Amino Acid Designator 90 Wrong Amino Acid Designator 91 Wrong Amino Acid Designator 92 Entered (18) and Cale. Seq. Length (0) differ 107 Wrong Amino Acid Designator 108 Wrong Amino Acid Designator 119 Wrong Amino Acid Designator 110 Wrong Amino Acid Designator 110 Wrong Amino Acid Designator 111 Entered (18) and Cale. Seq. Length (0) differ 112 Wrong Amino Acid Designator 113 Entered (18) and Cale. Seq. Length (0) differ 114 Wrong Amino Acid Designator 115 Entered (15) and Cale. Seq. Length (0) differ 116 Wrong Amino Acid Designator 117 Wrong Amino Acid Designator 118 Entered (18) and Cale. Seq. Length (0) differ 119 Wrong Amino Acid Designator 110 Wrong Amino Acid Designator 110 Wrong Amino Acid Designator 111 Entered (18) and Cale. Seq. Length (0) differ 112 Entered (18) and Cale. Seq. Length (0) differ 113 Wrong Amino Acid Designator 114 Wrong Amino Acid Designator 115 Entered (18) and Cale. Seq. Length (0) differ 116 Wrong Amino Acid Designator 117 Wrong Amino Acid Designator 118 Entered (18) and Cale. Seq. Length (0) differ 119 Entered (18) and Cale. Seq. Length (0) differ 110 Wrong Amino Acid Designator 111 Wrong Amino Acid Designator 112 Entered (18) and Cale. Seq. Length (0) differ 113 Wrong Amino Acid Designator 114 Wrong Amino Acid Designator 115 Entered (18) and Cale. Seq. Length (0) differ 116 Wrong Amino Acid Designator 117 Wrong Amino Acid Designator 118 Wrong Amino Acid Designator 119 Wrong Amino Acid Designator 119 Wrong Amino Acid Designator 110 Wrong Amino Acid Designator 110 Wrong Amino Acid Designator 111 Wrong Amino Acid Designator 112 Entered (18) and Cale. Seq. Length (0) differ 113 Wrong Amino Acid Designator 114 Wrong Amino Acid Designator 115 Entered (18) and Cale. Seq. Length (0) differ 116 Wrong Amino Acid Designator 117 Wrong Amino Ac	Line	Error	Original Text
50 Wrong Amino Acid Designator 51 Wrong Amino Acid Designator 52 Wrong Amino Acid Designator 53 Entered (18) and Cale. Seq. Length (0) differ 54 Wrong Amino Acid Designator 55 Entered (18) and Cale. Seq. Length (0) differ 56 Wrong Amino Acid Designator 57 Entered (18) and Cale. Seq. Length (0) differ 58 Wrong Amino Acid Designator 59 Wrong Amino Acid Designator 50 Wrong Amino Acid Designator 50 Wrong Amino Acid Designator 51 Wrong Amino Acid Designator 52 Entered (18) and Cale. Seq. Length (0) differ 53 Wrong Amino Acid Designator 54 Wrong Amino Acid Designator 55 Entered (18) and Cale. Seq. Length (0) differ 56 Wrong Amino Acid Designator 57 Wrong Amino Acid Designator 58 Entered (18) and Cale. Seq. Length (0) differ 59 Wrong Amino Acid Designator 50 Wrong Amino Acid Designator 51 Entered (18) and Cale. Seq. Length (0) differ 50 Wrong Amino Acid Designator 51 Entered (18) and Cale. Seq. Length (0) differ 51 Wrong Amino Acid Designator 52 Entered (18) and Cale. Seq. Length (0) differ 53 Wrong Amino Acid Designator 54 Wrong Amino Acid Designator 55 Entered (18) and Cale. Seq. Length (0) differ 56 Wrong Amino Acid Designator 57 Entered (18) and Cale. Seq. Length (0) differ 58 Wrong Amino Acid Designator 59 Wrong Amino Acid Designator 50 Wrong Amino Acid Designator 51 Entered (18) and Cale. Seq. Length (0) differ 52 Wrong Amino Acid Designator 53 Entered (18) and Cale. Seq. Length (0) differ 54 Wrong Amino Acid Designator 55 Entered (18) and Cale. Seq. Length (0) differ 56 Wrong Amino Acid Designator 57 Entered (18) and Cale. Seq. Length (0) differ 58 Wrong Amino Acid Designator 59 Entered (18) and Cale. Seq. Length (0) differ 59 Wrong Amino Acid Designator 50 Wrong Amino Acid Designator 50 Wrong Amino Acid Designator 50 Wrong Amino Acid Designator 51 Wrong Amino Acid Designator 52 Entered (18) and Cale. Seq. Length (0) differ 59 Wrong Amino Acid Designator 50 Wrong Amino Acid Designator 50 Wrong Amino Acid Designator 50 Wrong Amino Acid Designator 51 Wrong Amino Acid Designator 52 Wrong Amino Acid Designator 53 W	20	Wrong application Serial Number	(A) APPLICATION NUMBER: NONE
So Wrong Amino Acid Designator Wrong Amino Acid Designator Wrong Amino Acid Designator ProValThr:GlnAsp Wrong Amino Acid Designator Refered (18) and Cale. Seq. Length (0) differ Wrong Amino Acid Designator Wrong			
52 Wrong Amino Acid Designator 58 Entered (18) and Cale. Seq. Length (0) differ 69 Wrong Amino Acid Designator 71 Wrong Amino Acid Designator 72 Entered (18) and Cale. Seq. Length (0) differ 73 Wrong Amino Acid Designator 74 Wrong Amino Acid Designator 75 Entered (18) and Cale. Seq. Length (0) differ 76 Wrong Amino Acid Designator 77 Wrong Amino Acid Designator 78 Wrong Amino Acid Designator 79 Wrong Amino Acid Designator 79 Wrong Amino Acid Designator 71 Wrong Amino Acid Designator 71 Wrong Amino Acid Designator 72 Wrong Amino Acid Designator 73 Entered (18) and Cale. Seq. Length (0) differ 74 Wrong Amino Acid Designator 75 Wrong Amino Acid Designator 76 Wrong Amino Acid Designator 77 Entered (18) and Cale. Seq. Length (0) differ 78 Wrong Amino Acid Designator 79 Wrong Amino Acid Designator 70 Wrong Amino Acid Designator 71 Wrong Amino Acid Designator 72 Entered (18) and Cale. Seq. Length (0) differ 73 Wrong Amino Acid Designator 74 Wrong Amino Acid Designator 75 Entered (18) and Cale. Seq. Length (0) differ 76 Wrong Amino Acid Designator 77 Entered (18) and Cale. Seq. Length (0) differ 78 Wrong Amino Acid Designator 78 Entered (18) and Cale. Seq. Length (0) differ 79 Wrong Amino Acid Designator 70 Wrong Amino Acid Designator 71 Wrong Amino Acid Designator 71 Wrong Amino Acid Designator 72 Entered (18) and Cale. Seq. Length (0) differ 73 Wrong Amino Acid Designator 74 Wrong Amino Acid Designator 75 Entered (18) and Cale. Seq. Length (0) differ 76 Wrong Amino Acid Designator 77 Wrong Amino Acid Designator 78 Entered (18) and Cale. Seq. Length (0) differ 79 Wrong Amino Acid Designator 70 Wrong Amino Acid Designator 71 Wrong Amino Acid Designator 71 Wrong Amino Acid Designator 72 Wrong Amino Acid Designator 73 Wrong Amino Acid Designator 74 Wrong Amino Acid Designator 75 Entered (18) and Cale. Seq. Length (0) differ 76 Wrong Amino Acid Designator 77 Wrong Amino Acid Designator 78 Entered (18) and Cale. Seq. Length (0) differ 79 Wrong Amino Acid Designator 70 Wrong Amino Acid Designator 71 Wrong Amino Acid Designa			
58 Entered (18) and Cale. Seq. Length (0) differ 69 Wrong Amino Acid Designator 71 Wrong Amino Acid Designator 72 Entered (18) and Cale. Seq. Length (0) differ 88 Wrong Amino Acid Designator 90 Wrong Amino Acid Designator 90 Wrong Amino Acid Designator 91 Wrong Amino Acid Designator 90 Wrong Amino Acid Designator 91 Wrong Amino Acid Designator 92 Wrong Amino Acid Designator 93 Wrong Amino Acid Designator 94 Wrong Amino Acid Designator 95 Entered (18) and Cale. Seq. Length (0) differ 96 Wrong Amino Acid Designator 115 Entered (18) and Cale. Seq. Length (0) differ 116 Wrong Amino Acid Designator 117 Wrong Amino Acid Designator 118 Entered (15) and Cale. Seq. Length (0) differ 119 Wrong Amino Acid Designator 119 Wrong Amino Acid Designator 110 Wrong Amino Acid Designator 110 Wrong Amino Acid Designator 111 Entered (18) and Cale. Seq. Length (0) differ 112 Entered (18) and Cale. Seq. Length (0) differ 113 Wrong Amino Acid Designator 114 Wrong Amino Acid Designator 115 Entered (18) and Cale. Seq. Length (0) differ 116 Wrong Amino Acid Designator 117 Wrong Amino Acid Designator 118 Entered (18) and Cale. Seq. Length (0) differ 119 Entered (18) and Cale. Seq. Length (0) differ 110 Wrong Amino Acid Designator 111 Wrong Amino Acid Designator 112 Entered (18) and Cale. Seq. Length (0) differ 113 Wrong Amino Acid Designator 114 Wrong Amino Acid Designator 115 Entered (18) and Cale. Seq. Length (0) differ 116 Wrong Amino Acid Designator 117 Wrong Amino Acid Designator 118 Wrong Amino Acid Designator 119 Wrong Amino Acid Designator 119 Wrong Amino Acid Designator 110 Wrong Amino Acid Designator 110 Wrong Amino Acid Designator 111 Wrong Amino Acid Designator 112 Entered (18) and Cale. Seq. Length (0) differ 113 Wrong Amino Acid Designator 114 Wrong Amino Acid Designator 115 Entered (18) and Cale. Seq. Length (0) differ 115 Entered (18) and Cale. Seq. Length (0) differ 116 Wrong Amino Acid Designator 117 Wrong Amino Acid Designator 118 Wrong Amino Acid Designator 119 Wrong Amino Acid Designator 110 Wrong Amino Acid Designator			
98 Wrong Amino Acid Designator 71 Wrong Amino Acid Designator 72 Entered (18) and Cale. Seq. Length (0) differ 73 By Wrong Amino Acid Designator 74 Entered (18) and Cale. Seq. Length (0) differ 75 Wrong Amino Acid Designator 76 Entered (18) and Cale. Seq. Length (0) differ 77 Wrong Amino Acid Designator 78 Wrong Amino Acid Designator 89 Wrong Amino Acid Designator 81 Entered (18) and Cale. Seq. Length (0) differ 81 Wrong Amino Acid Designator 82 Wrong Amino Acid Designator 83 Wrong Amino Acid Designator 84 Wrong Amino Acid Designator 85 Wrong Amino Acid Designator 86 Wrong Amino Acid Designator 87 Wrong Amino Acid Designator 88 Wrong Amino Acid Designator 89 Wrong Amino Acid Designator 89 Wrong Amino Acid Designator 80 Wrong Amino Acid Designator 81 Entered (18) and Cale. Seq. Length (0) differ 81 Wrong Amino Acid Designator 82 Entered (18) and Cale. Seq. Length (0) differ 83 Wrong Amino Acid Designator 84 Wrong Amino Acid Designator 85 Entered (18) and Cale. Seq. Length (0) differ 86 Wrong Amino Acid Designator 87 Entered (18) and Cale. Seq. Length (0) differ 88 Wrong Amino Acid Designator 88 Wrong Amino Acid Designator 89 Wrong Amino Acid Designator 80 Entered (18) and Cale. Seq. Length (0) differ 80 Wrong Amino Acid Designator 81 Wrong Amino Acid Designator 82 Entered (18) and Cale. Seq. Length (0) differ 83 Wrong Amino Acid Designator 84 Wrong Amino Acid Designator 85 Entered (18) and Cale. Seq. Length (0) differ 86 Wrong Amino Acid Designator 87 Entered (18) and Cale. Seq. Length (0) differ 88 Wrong Amino Acid Designator 89 Wrong Amino Acid Designator 80 Entered (18) and Cale. Seq. Length (0) differ 80 Wrong Amino Acid Designator 81 Wrong Amino Acid Designator 82 Entered (18) and Cale. Seq. Length (0) differ 83 Wrong Amino Acid Designator 84 Wrong Amino Acid Designator 85 Entered (18) and Cale. Seq. Length (0) differ 86 Wrong Amino Acid Designator 87 Entered (18) and Cale. Seq. Length (0) differ 88 Wrong Amino Acid Designator 89 Wrong Amino Acid Designator 80 Entered (18) and Cale. Seq. Length (0) differ 8			•
77 Entered (18) and Cale. Seq. Length (0) differ 88 Wrong Amino Acid Designator 90 Wrong Amino Acid Designator 91 Wrong Amino Acid Designator 92 Entered (18) and Cale. Seq. Length (0) differ 107 Wrong Amino Acid Designator 118 Entered (18) and Cale. Seq. Length (0) differ 119 Wrong Amino Acid Designator 110 Wrong Amino Acid Designator 111 Entered (18) and Cale. Seq. Length (0) differ 110 Wrong Amino Acid Designator 111 Entered (17) and Cale. Seq. Length (0) differ 112 Wrong Amino Acid Designator 113 Entered (17) and Cale. Seq. Length (0) differ 114 Wrong Amino Acid Designator 115 Entered (15) and Cale. Seq. Length (0) differ 115 Wrong Amino Acid Designator 116 Wrong Amino Acid Designator 117 Wrong Amino Acid Designator 118 Wrong Amino Acid Designator 119 Entered (18) and Cale. Seq. Length (0) differ 119 Entered (18) and Cale. Seq. Length (0) differ 110 Wrong Amino Acid Designator 111 Entered (18) and Cale. Seq. Length (0) differ 112 Entered (18) and Cale. Seq. Length (0) differ 113 Wrong Amino Acid Designator 114 Wrong Amino Acid Designator 115 Entered (18) and Cale. Seq. Length (0) differ 116 Wrong Amino Acid Designator 117 Wrong Amino Acid Designator 118 Wrong Amino Acid Designator 119 Wrong Amino Acid Designator 110 Wrong Amino Acid Designator 110 Wrong Amino Acid Designator 111 Wrong Amino Acid Designator 112 Entered (18) and Cale. Seq. Length (0) differ 113 Wrong Amino Acid Designator 114 Wrong Amino Acid Designator 115 Entered (18) and Cale. Seq. Length (0) differ 115 Wrong Amino Acid Designator 116 Wrong Amino Acid Designator 117 Wrong Amino Acid Designator 118 Wrong Amino Acid Designator 119 Wrong Amino Acid Designator 119 Wrong Amino Acid Designator 110 Wrong Amino Acid Designator 110 Wrong Amino Acid Designator 111 Wrong Amino Acid Designator 112 Entered (18) and Cale. Seq. Length (0) differ 113 Wrong Amino Acid Designator 114 Wrong Amino Acid Designator 115 Entered (18) and Cale. Seq. Length (0) differ 118 Wrong Amino Acid Designator 119 Wrong Amino Acid Designator 119 Wrong Amino Acid Designator 110			
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550 Entered (18) and Calc. Seq. Length (0) differ 561 Wrong Amino Acid Designator 563 Wrong Amino Acid Designator 569 Entered (18) and Calc. Seq. Length (0) differ 580 Wrong Amino Acid Designator 582 Wrong Amino Acid Designator 588 Entered (18) and Calc. Seq. Length (0) differ 589 Wrong Amino Acid Designator 580 Wrong Amino Acid Designator 580 Wrong Amino Acid Designator 581 Entered (18) and Calc. Seq. Length (0) differ 580 Wrong Amino Acid Designator 581 Entered (18) and Calc. Seq. Length (0) differ 582 Wrong Amino Acid Designator 583 Entered (18) and Calc. Seq. Length (0) differ 684 Wrong Amino Acid Designator 685 Entered (18) and Calc. Seq. Length (0) differ 686 Wrong Amino Acid Designator 687 Entered (18) and Calc. Seq. Length (0) differ 688 Wrong Amino Acid Designator 688 Wrong Amino Acid Designator 689 Wrong Amino Acid Designator 680 Wrong Amin			
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588 Entered (18) and Calc. Seq. Length (0) differ 599 Wrong Amino Acid Designator ProAlaLeuValGlnGlyIleLeuGluArgValValAsp 601 Wrong Amino Acid Designator GlyProThrProHis 607 Entered (18) and Calc. Seq. Length (0) differ 619 Wrong Amino Acid Designator ArgMetThrLeuValPheGlySerArgArgProAspGlu 621 Wrong Amino Acid Designator AspHisIleTyrGln 627 Entered (18) and Calc. Seq. Length (0) differ 638 Wrong Amino Acid Designator AsnAsnAsnValGluLysAlaProSerAlaThrSerSer 640 Wrong Amino Acid Designator ProValThrGlnAsp			
599Wrong Amino Acid DesignatorProAlaLeuValGlnGlyIleLeuGluArgValValAsp601Wrong Amino Acid DesignatorGlyProThrProHis607Entered (18) and Calc. Seq. Length (0) differ(A) LENGTH: 18619Wrong Amino Acid DesignatorArgMetThrLeuValPheGlySerArgArgProAspGlu621Wrong Amino Acid DesignatorAspHisIleTyrGln627Entered (18) and Calc. Seq. Length (0) differ(A) LENGTH: 18638Wrong Amino Acid DesignatorAsnAsnAsnValGluLysAlaProSerAlaThrSerSer640Wrong Amino Acid DesignatorProValThrGlnAsp			(A) LENGTH: 18
607 Entered (18) and Calc. Seq. Length (0) differ 619 Wrong Amino Acid Designator ArgMetThrLeuValPheGlySerArgArgProAspGlu 621 Wrong Amino Acid Designator AspHisIleTyrGln 627 Entered (18) and Calc. Seq. Length (0) differ 638 Wrong Amino Acid Designator AsnAsnValGluLysAlaProSerAlaThrSerSer 640 Wrong Amino Acid Designator ProValThrGlnAsp			
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Wrong Amino Acid Designator ArgMetThrLeuValPheGlySerArgArgProAspGlu AspHisIleTyrGln AspHisIleTyrGln Calc Entered (18) and Calc. Seq. Length (0) differ Wrong Amino Acid Designator AspAsnAsnValGluLysAlaProSerAlaThrSerSer AsnAsnAsnValGluLysAlaProSerAlaThrSerSer ProValThrGlnAsp			
621 Wrong Amino Acid Designator AspHisIleTyrGln 627 Entered (18) and Calc. Seq. Length (0) differ (A) LENGTH: 18 638 Wrong Amino Acid Designator AsnAsnValGluLysAlaProSerAlaThrSerSer 640 Wrong Amino Acid Designator ProValThrGlnAsp			
627 Entered (18) and Calc. Seq. Length (0) differ 638 Wrong Amino Acid Designator 640 Wrong Amino Acid Designator 640 ProValThrGlnAsp (A) LENGTH: 18 AsnAsnAsnValGluLysAlaProSerAlaThrSerSer ProValThrGlnAsp			
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Wrong Amino Acid Designator ProValThrGlnAsp			
			ProValThrGlnAsp
	646		(A) LENGTH: 18

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Line	Error	Original Text
657	Wrong Amino Acid Designator	AsnAsnAsnValLysLysThrProSerAlaValLeuSer
659	Wrong Amino Acid Designator	ProThrIleGlnAsp
665	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
676	Wrong Amino Acid Designator	AsnAsnAsnValGluLysThrProGlyAlaIleProSer
678	Wrong Amino Acid Designator	ProThrThrGlnAsp
684	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
695	Wrong Amino Acid Designator	ValGluLysAlaProSerAlaThrSerSerProValThr
697	Wrong Amino Acid Designator Wrong Amino Acid Designator	GlnAsp
703	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
714	Wrong Amino Acid Designator	AlaProSerAlaThrSerSerProValThrGlnAsp
720	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
731		AlaThrSerSerProValThrGlnAsp
737	Wrong Amino Acid Designator Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
		SerProValThrGlnAsp
748 754	Wrong Amino Acid Designator Entered (15) and Cale Sea, Length (0) differ	
754 765	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
765 767	Wrong Amino Acid Designator	AsnAsnAsnValGluLysAlaProSerAlaThrSerSer
767	Wrong Amino Acid Designator	ProVal
773	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
784	Wrong Amino Acid Designator	AsnAsnAsnValGluLysAlaProSerAlaThrSer
790	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
801	Wrong Amino Acid Designator	AsnAsnAsnValGluLysAlaProSer
807	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
818	Wrong Amino Acid Designator	AsnAsnAsnValGluLys
824	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
835	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
837	Wrong Amino Acid Designator	SerLysGlnGlnAsn
843	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
854	Wrong Amino Acid Designator	ThrGlnAspAspLeuGlnTyrHisAsnLeuSerLysGln
856	Wrong Amino Acid Designator	GlnAsn
862	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
873	Wrong Amino Acid Designator	AspLeuGlnTyrHisAsnLeuSerLysGlnGlnAsn
881	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
892	Wrong Amino Acid Designator	TyrHisAsnLeuSerLysGlnGlnAsn
898	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
909	Wrong Amino Acid Designator	LeuSerLysGlnGlnAsn
915	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
926	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
928	Wrong Amino Acid Designator	SerLys
934	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
945	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGlnTyrHisAsn
951	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
962	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGln
968	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
979	Wrong Amino Acid Designator	SerProValThrGlnAsp
986	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
997	Wrong Amino Acid Designator	ProAlaLeuValGlnGlyIleLeuGluArgValValAsp
999	Wrong Amino Acid Designator	GlyProThrProHis
1005	Entered (19) and Calc. Seq. Length (0) differ	(A) LENGTH: 19

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Line	Error	Original Text
1016	Wrong Amino Acid Designator	ProGlyLeuValGluAlaLeuLeuSerArgValGluAsp
1018	Wrong Amino Acid Designator	ProProAlaProThrGlu
1024	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
1036	Wrong Amino Acid Designator	ValGlnGlyIleLeuGluArgValValAspGlyProThr
1038	Wrong Amino Acid Designator	ProHis
1044	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
1055	Wrong Amino Acid Designator	IleLeuGluArgValValAspGlyProThrProHis
1061	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1072	Wrong Amino Acid Designator	ArgValValAspGlyProThrProHis
1078	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
1089	Wrong Amino Acid Designator	AspGlyProThrProHis
1095	Entered (14) and Calc. Seq. Length (1) differ	(A) LENGTH: 14
1106	Wrong Amino Acid Designator	ProAlaLeuValGlnGlylleLeuGluArgValValAsp
1113	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
1124	Wrong Amino Acid Designator	ProAlaLeuValGlnGlyIleLeuGluArgValVal
1130	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1141	Wrong Amino Acid Designator	ProAlaLeuValGlnGlyIleLeuGlu
1147	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
1158	Wrong Amino Acid Designator	ProAlaLeuValGInGly
1164	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
1175	Wrong Amino Acid Designator	GlylleValProPheArgSerPheTrpGlnGlnArgLeu
1177	Wrong Amino Acid Designator	His Asp Ser Gln His
1183	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
1194	Wrong Amino Acid Designator	GlyIleAlaProPheArgSerPheTrpGlnGlnArgGln
1196	Wrong Amino Acid Designator	PheAspIleGlnHis
1202	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
1213	Wrong Amino Acid Designator	GlyIleAlaProPheArgGlyPheTrpGlnGluArgLeu
1215	Wrong Amino Acid Designator	HisAsp
1221	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
1232	Wrong Amino Acid Designator	ProPheArgSerPheTrpGlnGlnArgLeuHisAspSer
1234	Wrong Amino Acid Designator	GlnHis
1240	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
1251	Wrong Amino Acid Designator	SerPheTrpGlnGlnArgLeuHisAspSerGlnHis
1257	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1268	Wrong Amino Acid Designator	GlnGlnArgLeuHisAspSerGlnHis
1274	Entered (5) and Calc. Seq. Length (0) differ	(A) LENGTH: 5
1285	Wrong Amino Acid Designator	HisAspSerGlnHis
1291	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
1302	Wrong Amino Acid Designator	GlyIleValProPheArgSerPheTrpGlnGlnArgLeu
1304	Wrong Amino Acid Designator	HisAsp
1310	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
1321	Wrong Amino Acid Designator	GlyIleValProPheArgSerPheTrpGlnGlnArg
1327	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1338	Wrong Amino Acid Designator	GlyIleValProPheArgSerPheTrp
1344	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
1355	Wrong Amino Acid Designator	GlyIleValProPheArg
1361	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
1372	Wrong Amino Acid Designator	ArgMetThrLeuValPheGlySerArgArgProAspGlu

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Line	Error	Original Text
1374	Wrong Amino Acid Designator	AspHisIleTyrGln
1380	Entered (17) and Calc. Seq. Length (0) differ	(A) LENGTH: 17
1391	Wrong Amino Acid Designator	MetThrLeuValPheGlySerArgSerSerGlnLeuAsp
1393	Wrong Amino Acid Designator	HisLeuTyrArg
1399	Entered (17) and Calc. Seq. Length (0) differ	(A) LENGTH: 17
1410	Wrong Amino Acid Designator	MetValLeuValPheGlySerArgGlnSerLysIleAsp
1412	Wrong Amino Acid Designator	HislleTyrArg
1418	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15
1429	Wrong Amino Acid Designator	LeuValPheGlySerArgArgProAspGluAspHisIle
1431	Wrong Amino Acid Designator	TyrGln
1437	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
1448	Wrong Amino Acid Designator	GlySerArgArgProAspGluAspHisIleTyrGln
1456	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1467	Wrong Amino Acid Designator	ÀrgProAspGluAspHisIleTyrGln
1473	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
1484	Wrong Amino Acid Designator	GluAspHisIleTyrGln
1490	Entered (15) and Calc. Seq. Length (0) differ	(A) LÊNGTH: 15
1501	Wrong Amino Acid Designator	ArgMetThrLeuValPheGlySerArgArgProAspGlu
1503	Wrong Amino Acid Designator	AspHis
1509	Entered (11) and Calc. Seq. Length (0) differ	(A) LENGTH: 11
1520	Wrong Amino Acid Designator	ArgMetThrLeuValPheGlySerArgArgPro
1526	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1537	Wrong Amino Acid Designator	ArgMetThrLeuValPheGlySerArg-amide
1543	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
1554	Wrong Amino Acid Designator	ArgMetThrLeuValPhe-amide
1561	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
1572	Wrong Amino Acid Designator	ThrGlnAspAspLeuGlnTyrHisAsnLeuSerLys
1578	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1589	Wrong Amino Acid Designator	ValGlnGlyIleLeuGluArgValVal
1595	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
1606	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
1608	Wrong Amino Acid Designator	SerLysGlnGlnAsn
1614	Entered (5) and Calc. Seq. Length (0) differ	(A) LENGTH: 5
1625	Wrong Amino Acid Designator	GlnAspAspLeuGln
1631	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
1642	Wrong Amino Acid Designator	ThrGlnAspAspLeuGln
1648	Entered (7) and Calc. Seq. Length (0) differ	(A) LENGTH: 7
1659	Wrong Amino Acid Designator	ValThrGlnAspAspLeuGln
1667	Entered (8) and Calc. Seq. Length (0) differ	(A) LENGTH: 8
1678	Wrong Amino Acid Designator	ProValThrGlnAspAspLeuGln
1684	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1695	Wrong Amino Acid Designator	SerProValThrGinAspAspLeuGln
1701	Entered (5) and Calc. Seq. Length (0) differ	(A) LENGTH: 5
1712	Wrong Amino Acid Designator	ThrGlnAspAspLeu
1719	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
1730	Wrong Amino Acid Designator	ValThrGlnAspAspLeu
1736	Entered (7) and Calc. Seq. Length (0) differ	(A) LENGTH: 7
1747	Wrong Amino Acid Designator	ProValThrGlnAspAspLeu

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Line	Error	Original Text
1753	Entered (8) and Calc. Seq. Length (0) differ	(A) LENGTH: 8
1764	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeu
1771	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1782	Wrong Amino Acid Designator	SerSerProValThrGlnAspAspLeu
1788	Entered (5) and Calc. Seq. Length (0) differ	(A) LENGTH: 5
1799	Wrong Amino Acid Designator	ValThrGlnAspAsp
1805	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
1816	Wrong Amino Acid Designator	ProValThrGlnAspAsp
1823	Entered (7) and Calc. Seq. Length (0) differ	(A) LENGTH: 7
1834	Wrong Amino Acid Designator	SerProValThrGlnAspAsp
1840	Entered (8) and Calc. Seq. Length (0) differ	(A) LENGTH: 8
1851	Wrong Amino Acid Designator	SerSerProValThrGlnAspAsp
1857	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
1868	Wrong Amino Acid Designator	ThrSerSerProValThrGlnAspAsp
1875	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
1886	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
		SerLysGlnGlnAsn
1888 1894	Wrong Amino Acid Designator Entered (15) and Cala Sea Length (0) differ	(A) LENGTH: 15
	Entered (15) and Calc. Seq. Length (0) differ	
1905	Wrong Amino Acid Designator	ThrGlnAspAspLeuGlnTyrHisAsnLeuSerLysGln GlnAsn
1907	Wrong Amino Acid Designator	(A) LENGTH: 12
1913	Entered (12) and Calc. Seq. Length (0) differ	` '
1925	Wrong Amino Acid Designator	AspLeuGlnTyrHisAsnLeuSerLysGlnGlnAsn
1931	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9 Turlio A on Lou Sort vo Cin Cin A on
1942	Wrong Amino Acid Designator	TyrHisAsnLeuSerLysGlnGlnAsn
1948	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
1959	Wrong Amino Acid Designator	LeuSerLysGlnGlnAsn
1965	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH: 15 See Pro VolThy Cla A on A on Lou Cla Turthic A on Lou
1976	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGlnTyrHisAsnLeu
1978	Wrong Amino Acid Designator	SerLys
1984	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH: 12
1995	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGlnTyrHisAsn
2001	Entered (9) and Calc. Seq. Length (0) differ	(A) LENGTH: 9
2012	Wrong Amino Acid Designator	SerProValThrGlnAspAspLeuGln
2018	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
2030	Wrong Amino Acid Designator	SerProValThrGlnAsp
2036	Entered (10) and Calc. Seq. Length (0) differ	(A) LENGTH: 10
2047	Wrong Amino Acid Designator	ThrSerSerProValThrGlnAspAspLeu
2053	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18
2064	Wrong Amino Acid Designator	ProAlaLeuValGlnGlyIleLeuGluArgValValAsp
2066	Wrong Amino Acid Designator	GlyProThrProHis
2072	Entered (5) and Calc. Seq. Length (0) differ	(A) LENGTH: 5
2084	Wrong Amino Acid Designator	LeuGluArgValVal
2090	Entered (6) and Calc. Seq. Length (0) differ	(A) LENGTH: 6
2101	Wrong Amino Acid Designator	IleLeuGluArgValVal
2107	Entered (7) and Calc. Seq. Length (0) differ	(A) LENGTH: 7
2118	Wrong Amino Acid Designator	GlylleLeuGluArgValVal
2124	Entered (8) and Calc. Seq. Length (0) differ	(A) LENGTH: 8
2136	Wrong Amino Acid Designator	GlnGlylleLeuGluArgValVal

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/833,506A

DATE: 03/29/1999 TIME: 08:48:27

Line	Error	Original Text
2142 2153 2159 2170 2176 2188 2194 2205	Entered (9) and Calc. Seq. Length (0) differ Wrong Amino Acid Designator Entered (5) and Calc. Seq. Length (0) differ Wrong Amino Acid Designator Entered (6) and Calc. Seq. Length (0) differ Wrong Amino Acid Designator Entered (7) and Calc. Seq. Length (0) differ Wrong Amino Acid Designator Wrong Amino Acid Designator	(A) LENGTH: 9 ValGlnGlylleLeuGluArgValVal (A) LENGTH: 5 IleLeuGluArgVal (A) LENGTH: 6 GlylleLeuGluArgVal (A) LENGTH: 7 GlnGlylleLeuGluArgVal
2211 2222 2228 2240 2246 2257 2263 2274 2280 2292	Entered (8) and Calc. Seq. Length (0) differ Wrong Amino Acid Designator Entered (9) and Calc. Seq. Length (0) differ Wrong Amino Acid Designator Entered (5) and Calc. Seq. Length (0) differ Wrong Amino Acid Designator Entered (6) and Calc. Seq. Length (0) differ Wrong Amino Acid Designator Entered (7) and Calc. Seq. Length (0) differ Wrong Amino Acid Designator Entered (7) and Calc. Seq. Length (0) differ Wrong Amino Acid Designator	(A) LENGTH: 8 ValGlnGlylleLeuGluArgVal (A) LENGTH: 9 LeuValGlnGlylleLeuGluArgVal (A) LENGTH: 5 GlylleLeuGluArg (A) LENGTH: 6 GlnGlylleLeuGluArg (A) LENGTH: 7 ValGlnGlylleLeuGluArg
2298 2310 2313	Entered (8) and Calc. Seq. Length (0) differ Wrong Amino Acid Designator Wrong Amino Acid Designator	(A) LENGTH: 8 LeuValGlnGlylleLeuGluArg ??